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 QY 181 THQISKDQYGLPDSGHTLGLFIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 Db 181 THQISKDQYGLPDSGHTLGLFIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 QY 241 HGEVCPAGWKPGSETIPDPAKLYFDKLN 271
 Db 241 HGEVCPAGWKPGSETIPDPAKLYFDKLN 271
 RESULT 2
 US-08-467-265-2
 ; Sequence 2, Application US/08467265
 ; Patent No. 6255079
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; GENTZ, Reiner
 ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,265
 ; FILING DATE: 06-Jun-1995
 ; CLASSIFICATION: <uninown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-456
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 271 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-08-467-265-2
 ; Query Match 100.0%; Score 1441; DB 4; Length 271;
 ; Best Local Similarity 100.0%; Pred. No. 2.5e-157; Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ; QY 1 MEALPLAATPDIGHRRLLLPLLFLPAGVQGWETEERTRREBECHYAGQVY 60
 ; 1 MEALPLAATPDIGHRRLLLPLLFLPAGVQGWETEERTRREBECHYAGQVY 60
 ; Db 1 MEALPLAATPDIGHRRLLLPLLFLPAGVQGWETEERTRREBECHYAGQVY 60
 ; QY 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 ; 1 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 ; Db 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 ; QY 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 ; Db 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 ; QY 121 TFVCPCTEIAGFDRLLEFRSINTEVACSVDSQFTHLAWINTPRRQGLGPIRPLSDL 180
 ; Db 121 TFVCPCTEIAGFDRLLEFRSINTEVACSVDSQFTHLAWINTPRRQGLGPIRPLSDL 180
 ; QY 181 THQISKDQYGLPDSGHTLGLFIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 ; Db 181 THQISKDQYGLPDSGHTLGLFIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 ; QY 241 HGEVCPAGWKPGSETIPDPAKLYFDKLN 271
 ; Db 241 HGEVCPAGWKPGSETIPDPAKLYFDKLN 271
 ; US-09-407-891-2
 ; Sequence 2, Application US/09407891
 ; Patent No. 6294114
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; GENTZ, Reiner
 ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/407,891
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-456
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 271 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-407-891-2
 ; Query Match 100.0%; Score 1441; DB 4; Length 271;
 ; Best Local Similarity 100.0%; Pred. No. 2.5e-157; Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Patent No. 6294164
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESSEE: STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/407, 891
 FILING DATE: 06-JUN-1995
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/4467, 265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 STRANDEDNESS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-407-891-15
 Query Match 51.4%; Score 740; DB 4; Length 198;
 Best Local Similarity 69.9%; Pred No 5.8e-77; Mismatches 135; Conservatism 25; MisMatches 33; Indels 0; Gaps 0;
 Qy 79 AKTSKPKAPWEGAVIIGEKFELKLTDYRGKYLVFFFPLDFVCPTEIAFGDRLEF 138
 Db 6 ARIGKPKAPDFKATAVVDGAFKEVLSDKYKVYVFLYFPPLDFVCPTEIAFNSRAEDF 65
 Qy 139 RSINTEVVACVSQDFTHLAWINTPRROGLGPIRIPSLDTHQISKDGYVLEDSHT 198
 Db 66 RKLIGCEVILGVGSVDSOENILAWINTPRKEGGIGPLNIPLUGDYLRLSDGYVILKTDEGIA 125
 Qy 199 LRGFLFIDDKGIGLIRQTLNDLPGRSVDETTLRIVQAFYTDKHEVCPAGWKPGSETIIP 258
 Db 126 YRGFLFIDKGIGVLRQITVNDLPGVGRSVDDEALRLVQAFQYTDKHEVCPAGWKPGSDTIK 185
 Qy 259 DPGKGLKVFDFKLN 271
 Db 186 NVDDSKEYFSKHN 198
 RESULT 7
 Sequence 17, Application US/08467265
 Patent No. 5985612
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 APPLICANT: Gantz, Reiner
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESSEE: STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467, 265
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-467-265-17
 Query Match 50.1%; Score 721.5; DB 2; Length 199;
 Best Local Similarity 68.8%; Pred No. 7.8e-75; Mismatches 132; Conservatism 27; MisMatches 32; Indels 1; Gaps 1;
 Matches 132; Conservatism 27; MisMatches 32; Indels 1; Gaps 1;
 Qy 79 AKTSKPKAPWEGAVIIGEKFELKLTDYRGKYLVFFFPLDFVCPTEIAFGDRLEF 137
 Db 66 AKIGYPPAPDFKATAVVDGAFKEVLSDKYKVYVFLYFPPLDFVCPTEIAFNSRAEDF 65
 Qy 198 TLRCLFIDDKGIGLIRQTLNDLPGRSVDETTLRIVQAFYTDKHEVCPAGWKPGSETIIP 257
 Db 126 SFRGLFIDDKGIGLIRQITVNDLPGVGRSVDDEALRLVQAFQYTDKHEVCPAGWKPGSDTIK 185
 Qy 258 PDPGKGLKVFDFKLN 269
 Db 185 PDWKSKKEVFSK 197
 RESULT 8
 Sequence 17, Application US/08467265
 Patent No. 6255079
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gentz, Reiner
 APPLICANT: Rosen, Craig A.
 APPLICANT: Gantz, Reiner
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESSEE: STUART & OLSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland

STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,265
 FILING DATE: 06-Jun-1995
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-08-467-265-17

Query Match 50.1%; Score 721.5; DB 4; Length 199;
 Best Local Similarity 68.8%; Pred. No. 7.8e-75;
 Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISKAPAPWEGTAVI-DGEEFKELKLTDYRGKYLVEFFYPLDFTWVCPTEITAFGDRLEE 137
 Db 6 AKIGKAPAPNKRATVAMPDQFDISLEYKGKVVFFYPLDFTWVCPTEITAFGDRADE 65

QY 138 FRSINTEVVACSVSDQFTHLAWINTERRQGGIPIPLSLDTLTHOSKDYCVLEDSGH 197
 Db 66 FKKINQCQVIGASVPHCFCHAWINTPKQGGIPIPLSLDPKRTIAQDGYVLADEGI 125

QY 198 TLRGFLIFTIDDKGILRQITLNDLPLVGRSVDTEIRLVAQFOYQFTDKHGEVCPAGWKPGSETTI 257
 Db 126 SFRGLIFTIDDKGILRQITLNDLPLVGRSVDTEIRLVAQFOYQFTDKHGEVCPAGWKPGSETTI 257

QY 258 PDPAGKLKYFDK 269
 Db 186 PDVNRKSEFSK 197

RESULT 9
 US-08-407-891-17
 Sequence 17, Application US/09407891
 Patent No. 6794164

GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Yu, Guo-Liang
 APPLICANT: Gantz, Reiner
 APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ADDRESS: 6 Becker Farm Road
 STREET: Roseland
 CITY: New Jersey
 STATE: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/299,162A
 FILING DATE: AUGUST 31, 1994
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: Oldenkamp, David J.
 REFERENCE/DOCKET NUMBER: 104-280

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-09-407-891-17

Query Match 50.1%; Score 721.5; DB 4; Length 199;
 Best Local Similarity 68.8%; Pred. No. 7.8e-75;
 Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

QY 79 AKISKAPAPWEGTAVI-DGEEFKELKLTDYRGKYLVEFFYPLDFTWVCPTEITAFGDRLEE 137
 Db 6 AKIGKAPAPNKRATVAMPDQFDISLEYKGKVVFFYPLDFTWVCPTEITAFGDRADE 65

QY 138 FRSINTEVVACSVSDQFTHLAWINTERRQGGIPIPLSLDTLTHOSKDYCVLEDSGH 197
 Db 66 FKKINQCQVIGASVPHCFCHAWINTPKQGGIPIPLSLDPKRTIAQDGYVLADEGI 125

QY 198 TLRGFLIFTIDDKGILRQITLNDLPLVGRSVDTEIRLVAQFOYQFTDKHGEVCPAGWKPGSETTI 257
 Db 126 SFRGLIFTIDDKGILRQITLNDLPLVGRSVDTEIRLVAQFOYQFTDKHGEVCPAGWKPGSETTI 257

QY 258 PDPAGKLKYFDK 269
 Db 186 PDVNRKSEFSK 197

RESULT 10
 US-08-299-162A-2
 Sequence 2, Application US/08299162A
 Patent No. 5610286

GENERAL INFORMATION:
 APPLICANT: Shau, Hungyi
 APPLICANT: Golub, Sidney H
 TITLE OF INVENTION: Natural Killer Cell Enhancing Factor
 NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
 ADDRESS: David J. Oldenkamp
 STREET: 2029 Century Park East, Suite 3800
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90067

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/299,162A
 FILING DATE: AUGUST 31, 1994
 CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
 NAME: Oldenkamp, David J.
 REFERENCE/DOCKET NUMBER: 104-280

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-788-5000
 TELEFAX: 310-277-1297

INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 199 amino acids
 TOPOLogy: linear
 MOLECULE TYPE: protein

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;
 TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 68.8%; Pred. No. 6.5e-74; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;
 TYPE: amino acid

MOLECULE TYPE: protein

Query Match, Best Local Similarity 68.8%; Pred. No. 6.5e-74; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 68.8%; Pred. No. 6.5e-74; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;
 TYPE: amino acid

MOLECULE TYPE: protein

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 1; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

TYPE: amino acid

US-08-299-162A-2

; MOLECULE TYPE: protein
 ; US-08-467-265-14
 Query Match, Best Local Similarity 49.5%; Score 713.5; DB 2; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;
 TYPE: amino acid
 Db 6 AKIGHPAPNPKATAVMPDGQFKDLSKDSYKGVVFFFYPLDFTFVCPTEIAFSDRAE 65
 Qy 138 FRSTNTEVVACSVDSQFTHLAWNTPRQGGGLPRLPLSDITHQTSKDYGVLEDSGH 197
 Db 66 FKKINQCVIGASVDSFHCLAWNTPKQGGGLPMNLYSPKRTAQDGVLKADEGI 125
 Qy 198 TRLSLFTIDDKGTLRQITWDLVGRSVDETLRLVQARQYTDKHEVCAGKPGSEII 257
 Db 126 SFRGLFIDDKGTLRQITWDLPCCRSVDETLRLVQARQFTDKHEVCAGKPGSEII 185
 Qy 258 PDAGKLYFKD 269
 Db 186 PDVPKTKEYFSK 197

RESULT 12
 US-08-467-265-14
 Sequence 14, Application US/08467265
 Patent No. 6253079

; GENERAL INFORMATION:
 APPLICANT: NL, Jian
 Yu, Guo-Liang
 Genthz, Reiner
 ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STUART & OSTEIN
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08467,265
 FILING DATE: 06-Jun-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:

; US-08-467-265-14

Query Match, Best Local Similarity 49.5%; Score 713.5; DB 4; Length 199;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISKPAPWEGTAVI-DGEEKEKLTDYRGKLVFFYPLDFIVCPBIIAGDRLEE 137
 Db 6 FKKLNQVIGASVDSFHCLAWNNTPKQKGPMNIPLVSDPKRTIAQDGVLKADEGI 125
 Db 6 AKIGHAPAPNPKATAVMPDGOFKDISLSYDQKGVYVFYPLDFIVCPBIIAGDRLEE 65

QY 138 FRSINTEVVACSVSDQFTTHAWINTPRQGGPTRIPLSLDTHQSKDQYGVVILEDSGH 197
 Db 66 FKKLNQVIGASVDSFHCLAWNNTPKQKGPMNIPLVSDPKRTIAQDGVLKADEGI 125
 Db 66 FKKLNQVIGASVDSFHCLAWNNTPKQKGPMNIPLVSDPKRTIAQDGVLKADEGI 125

QY 198 TLRGFLFIDDKGILRQITLNDLPGRSVDETLRLYQAFOYTDKIGEVCPAGWKPGSETII 257
 Db 126 SFRGLFLIDDKGILRQITLNDLPGRSVDETLRLYQAFOYTDKIGEVCPAGWKPGSETII 257
 Db 126 SFRGLFLIDDKGILRQITLNDLPGRSVDETLRLYQAFOYTDKIGEVCPAGWKPGSETII 185

QY 258 PDPAGKLKVYFDK 269
 Db 186 PDVPKTKEYFSK 197

RESULT 13
 US-09-407-891-14
 ; Sequence 14, Application US/09407891
 ; Patent No. 6294164
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, Jian
 ; APPLICANT: GENTZ, Reiner
 ; APPLICANT: YU, Guo-Liang
 ; APPLICANT: ROSEN, Craig A.
 ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; STREET: 6 Becker Farm Road
 ; STATE: NJ, USA
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/407,891
 ; ATTORNEY/AGENT INFORMATION:
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/467,265
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-456
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 199 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-407-891-14

Query Match 49.5%; Score 713.5%; DB 4%; Length 199;
 Best Local Similarity 68.8%; Pred. No. 6.5e-74; Length 257;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISKPAPWEGTAVI-DGEEKEKLTDYRGKLVFFYPLDFIVCPBIIAGDRLEE 137
 Db 66 VTOQAHPKGKPAVNGESEKSLDQPKGVYLFYPLDFIVCPBIIAGDRLEE 137
 Db 6 AKIGHAPAPNPKATAVMPDGOFKDISLSYDQKGVYVFYPLDFIVCPBIIAGDRLEE 65

QY 141 INTEVVACSVSDQFTTHAWINTPRQGGPTRIPLSLDTHQSKDQYGVVILEDSGH 200
 Db 126 VNCCEVVAWSVDSFHCLAWNNTPKQKGPMNIPLVSDPKRTIAQDGVLKADEGI 185
 Db 66 VTOQAHPKGKPAVNGESEKSLDQPKGVYLFYPLDFIVCPBIIAGDRLEE 125

QY 201 GLFIDDKGILRQITLNDLPGRSVDETLRLYQAFOYTDKIGEVCPAGWKPGSETII 260
 Db 186 GLFIDDPNGVYKHSVNDLPGVRSVETLRLYQAFOYTDKIGEVCPAGWKPGSETII 245

QY 261 AGKLKVYFDK 271

Db 246 TASKEYFEKVH 256

RESULT 15

US-08-467-265-16

; Sequence 15, Application US/08467265

Patent No. 6255079

GENERAL INFORMATION:

APPLICANT: Ni, Jian

Rosen, Craig A.

Yu, Guo-Liang

Gentz, Reiner

Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BATN, GILFILLAN, CECCHI,

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: #1.0, Version #1.30

APPLICATION NUMBER: US/08/467, 265

FILING DATE: 06-JUN-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: Linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-08-467-265-16

Query Match 47.8%; Score 689; DB 4; Length 257;

Best Local Similarity 64.4%; Pred. No. 6.3e-71; Mismatches 36; Indels 0; Gaps 0;

Matches 123; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

Qy 81 ISKAPWEGTAVIDGERFKEKLKDYRGKYLFFYFLDFTFVCPTEIAFGDRLEERS 140

Db 66 VVQHAPYFKGTAVNGEKFELSLDFKRYLFLFYPLDFTFVCPTEIAFGDRLEERS 125

Qy 141 INPFWVAVCSVDSQFTHLAWINPRQGIGPPIRIPULSLTQIISKDGYVLEDSGTLR 200

Db 126 VNCEVVAVSVDSHFLAWINTPRKNGGLGHWNITLSDITKQISROYGVILLESAGFLR 185

Qy 201 GUFIDDKGILRQITLNDLPGVRSVDETRLVQAFQVTDKHOEVCPAGWKPOSETTIPDP 260

Db 186 GUFIDDKGILRQITLNDLPGVRSVDETRLVQAFQVTDKHOEVCPAGWKPOSETTIPDP 245

Qy 261 AGKLKYFDKL 271

Db 246 TASKEYFEKVH 256

Search completed: January 17, 2003, 19:19:59
Job time : 17 secs

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OM protein - protein search, using SW model

Run on: January 17, 2003, 19:18:27 ; Search time 13 Seconds

Title: US-09-911-346-2
Perfect score: 1441
Sequence: 1 MEALPLAATPDPDGRHRRLL...GSETTIPDPAGKLVYFDKLN 271

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications_AA,*

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 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 11: /cgn2_6/ptodata/1/pubpaa/US10_NEWPUB.pep:*
 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
 13: /cgn2_6/ptodata/1/pubpaa/US60_NEWPUB.pep:*
 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1441	100.0	271	US-09-911-346-2
2	750.5	52.1	233	US-09-923-301-973
3	740	51.4	198	US-09-911-346-15
4	721.5	50.1	199	US-09-911-346-17
5	713.5	49.9	100	US-09-911-346-14
6	703	48.8	224	10 US-09-925-300-1537
7	689	47.8	257	10 US-09-911-346-16
8	598	41.5	926	9 US-09-991-496-128
9	598	41.5	955	9 US-09-991-496-127
10	598	41.5	982	9 US-09-991-496-95
11	598	41.5	982	10 US-09-894-923-95
12	598	41.5	1427	9 US-09-991-496-97
13	598	41.5	1427	10 US-09-894-923-97
14	598	41.5	1641	9 US-09-991-496-96
15	598	41.5	1641	10 US-09-894-923-96
16	591	41.0	446	9 US-10-025-380-112
17	591	41.0	446	10 US-09-922-217-1121
18	591	41.0	1464	9 US-09-011-896-1008
19	587	40.7	199	9 US-09-991-496-24

RESULT	1
SEQUENCE	US-09-911-346-2
PATENT NO.	US20020106323A1
GENERAL INFORMATION:	
APPLICANT:	NI, Jian Yu, Guo-Liang Gentz, Reiner Rosen, Craig A.
TITLE OF INVENTION:	NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES:	17
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	CARILLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET:	6 Becker Farm Road
CITY:	Roseland
STATE:	New Jersey
ZIP:	07068
COMPUTER READABLE FORM:	
MEDIUM TYPE:	Floppy disk
COMPUTER:	IBM PC compatible
OPERATING SYSTEM:	PC-DOS/MS-DOS
SOFTWARE:	PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:	
APPLICATION NUMBER:	US/09/911,346
FILING DATE:	24-Jul-2001
CLASSIFICATION:	<Unknown>
PRIOR APPLICATION DATA:	
APPLICATION NUMBER:	US 08/467,265
FILING DATE:	06-Jun-1995
ATTORNEY/AGENT INFORMATION:	
NAME:	Ferraro, Gregory D.
REGISTRATION NUMBER:	36,134
REFERENCE/DOCKET NUMBER:	325800-456
TELECOMMUNICATION INFORMATION:	
TELEPHONE:	201-994-1700
TELEFAX:	201-994-1744
INFORMATION FOR SEQ ID NO: 2:	
SEQUENCE CHARACTERISTICS:	
LENGTH:	271 amino acids
TYPE:	amino acid

TOPOLGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-911-346-2

Query Match 100.0%; Score 1441; DB 10; Length 271;
 Best Local Similarity 100.0%; Pred. No. 5.7e-139; Indels 0; Gaps 0;
 Matches 271; Conservative 0; Mismatches 0; Index 0;

Qy

Db

1 MEALPPLAATTPDGRHRRLLPLFLPAGAVQGVWETEERPRTRFECHTYAGQVY 60
 1 MELAPPLAATTPDGRHRRLLPLFLPAGAVQGVWETEERPRTRFECHTYAGQVY 60

Qy 61 PGEASRVSDAHSLSKAKISKAPYWGTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 61 PGEASRVSDAHSLSKAKISKAPYWGTAVIDGEFKEKLTDYRGKLVFFYPLDF 120

Qy 121 TFWCPTTEIAFGDRLEEFERSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 180
 121 TFWCPTTEIAFGDRLEEFERSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 180

Db 121 TFWCPTTEIAFGDRLEEFERSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 180
 181 THQISKDGYVYLRSQHSGHTLRLGKILRITLNDLPGVGSVDETLRLVQAFQYTDK 240
 181 THQISKDGYVYLRSQHSGHTLRLGKILRITLNDLPGVGSVDETLRLVQAFQYTDK 240

Qy 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271
 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271

Db 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271

RESULT 2

US-09-925-301-973

Sequence 973, Application US/09925301

Patent No. US2002010623A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925, 301

PRIOR APPLICATION NUMBER: PCT/US00/05882

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124, 270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 973

LENGTH: 233

TYPE: PRK

ORGANISM: Homo sapiens

FEATURE: SITE

LOCATION: (3)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match 52.1%; Score 750.5; DB 10; Length 233;
 Best Local Similarity 67.1%; Pred. No. 7.9e-69; Indels 1; Gaps 1;
 Matches 139; Conservative 27; Mismatches 40; Index 1;

Qy 64 ASRVSVDASHLSKAKISKAPYWGHTAVI-DGERKEKLTDYRGKLVFFYPLDFP 122
 64 ASRVSVDASHLSKAKISKAPYWGHTAVI-DGERKEKLTDYRGKLVFFYPLDFP 122

Db 25 ATCVGTADEKRNSSGNAKIGHPAPNFKTAYMPDQFDKTSLSDYKGKVVFFYPLDFT 84
 25 ATCVGTADEKRNSSGNAKIGHPAPNFKTAYMPDQFDKTSLSDYKGKVVFFYPLDFT 84

Qy 123 VCPTEIAFGDRLEERSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 182
 123 VCPTEIAFGDRLEERSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 182

Db 85 VCPTEIAFGDRLEERSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 144
 85 VCPTEIAFGDRLEERSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 144

Qy 183 QISKDGYVYLDSGHTLRLGFLPDTDKH 242
 183 QISKDGYVYLDSGHTLRLGFLPDTDKH 242

Db 145 TIAQDGYVLAKEDEGSFRGLFLIDDKGILRQITVNDLPGVGSVDETLRLVQAFQYTDK 204
 145 TIAQDGYVLAKEDEGSFRGLFLIDDKGILRQITVNDLPGVGSVDETLRLVQAFQYTDK 204

Qy 243 EVCPAGWKPGSETIIPDPAGKLKYFDKLN 269
 243 EVCPAGWKPGSETIIPDPAGKLKYFDKLN 269

RESULT 3
 US-09-911-346-15
 Sequence 15, Application US/09911346
 Patent No. US2002010623A1
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 ADDRESS: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 STREET: 6 Becker Farm Road
 CITY: Roseland
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068

Computer Readable Form:

Medium type: floppy disk

Computer: IBM PC compatible

Operating System: PC-DOS/MS-DOS

Software: Patentin Release #1.0, version #1.30

Current Application Data:

Application Number: US/09/911,346

Filing Date: 24-Jul-2001

Classification: <Unknown>

Prior Application Data:

Application Number: US 08/467,265

Filing Date: 06-JUN-1995

Attorney/Agent Information:

Name: Ferraro, Gregory D.

Registration Number: 35,134

Reference/DoCKET Number: 325800-456

Telecommunication Information:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

Information for Seq ID No: 15:

Sequence Characteristics:

Length: 198 amino acids

Type: amino acid

Strandness: <Unknown>

Topology: linear

Molecule Type: protein

Feature: SITE

Location: (3)

Other Information: Xaa equals any of the naturally occurring L-amino acids

US-09-911-346-15

Query Match 51.4%; Score 740; DB 10; Length 198;
 Best Local Similarity 69.9%; Pred. No. 7.3e-68; Indels 0; Gaps 0;
 Matches 135; Conservative 25; Mismatches 33; Index 0;

Qy 79 AKISKDGYVYLDSGHTLRLGFLPDTDKH 138
 79 AKISKDGYVYLDSGHTLRLGFLPDTDKH 138

Db 6 ARIGKAPDPDEKRNSSGNAKIGHPAPNFKTAYMPDQFDKTSLSDYKGKVVFFYPLDFT 65
 6 ARIGKAPDPDEKRNSSGNAKIGHPAPNFKTAYMPDQFDKTSLSDYKGKVVFFYPLDFT 65

Qy 139 RSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 198
 139 RSINTTWWVACSYSDFTPLWINTTTRQGGLGPIRPLSLD 198

Db 66 RKLGEVGLGVSDQFQNHAWLWINTTTRQGGLGPIRPLSLD 125
 66 RKLGEVGLGVSDQFQNHAWLWINTTTRQGGLGPIRPLSLD 125

Qy 199 LRGFLTDDKGILRQITVNDLPGVGSVDETLRLVQAFQYTDK 258
 199 LRGFLTDDKGILRQITVNDLPGVGSVDETLRLVQAFQYTDK 258

Db 126 YRGFLTDDKGILRQITVNDLPGVGSVDETLRLVQAFQYTDK 185
 126 YRGFLTDDKGILRQITVNDLPGVGSVDETLRLVQAFQYTDK 185

Qy 259 DPAGKLKYFDKLN 271
 259 DPAGKLKYFDKLN 271

Db 186 NVDSKEYFSKHN 198
 186 NVDSKEYFSKHN 198

Db 66 FSPSVSRFNLNECVLACSIDSBYAHQLQWTLQDRKKGGGLGTMIAIPMLADKTSIARSYGV 125 ; APPLICANT: Coler, Rhea
 Qy 191 YLEDSGHTLRGLIPIDDKGILRQITLNDLPLVGRSYDETRLVQAFQYTDKHEVCPAGWK 250 ; APPLICANT: Probst, Peter
 Db 126 LEESQVAYRGLFLIDPHGMLRQITVNDMPVGRSVEEVRLLEAFQFVEKHEVCPANWK 185 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 FILE REFERENCE: 210121.420C8 ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 CURRENT APPLICATION NUMBER: US/09/874, 923 ; CURRENT FILING DATE: 2001-06-04
 NUMBER OF SEQ ID NOS: 122 ; NUMBER OF SEQ ID NOS: 122
 SOFTWARE: FastSEQ for Windows Version 4.0 ; SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 97 ; SEQ ID NO 97
 LENGTH: 1427 ; LENGTH: 1427
 TYPE: PRT ; TYPE: PRT
 ORGANISM: Artificial Sequence ; ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple ; FEATURE: OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; OTHER INFORMATION: Leishmania antigens ; OTHER INFORMATION: Leishmania antigens
 ; US-09-991-496-97 ; US-09-991-496-97
 Query Match 41.5%; Score 598; DB 9; Length 1427;
 Best Local Similarity 54.0%; Pred. No. 3. 1e-52;
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;
 Qy 72 HSLHLSKAKISKPAPWEGAVI-DGEFKELKLTDYRGKYLVFFYPLDITFVCPEVIA 130 ; APPLICANT: Coler, Rhea
 Db 6 HMSCGNAKINSPPAPSFEEVALMPNGSKKISLSSYKGKWNVVLFFYPLDITFVCPEVIA 65 ; APPLICANT: Probst, Peter
 Qy 131 FGDRLEFRSNTTEVACVSQVSQFTLAWIWPRLGGSPTRILPSLTHQISKDYGV 190 ; APPLICANT: Webb, John R.
 Db 66 FSPSVSRFNLNECVLACSIDSBYAHQLQWTLQDRKKGGGLGTMIAIPMLADKTSIARSYGV 125 ; APPLICANT: Dillon, Devin C.
 Qy 191 YLEDSGHTLRGLIPIDDKGILRQITLNDLPLVGRSYDETRLVQAFQYTDKHEVCPAGWK 250 ; APPLICANT: Skeiky, Yasir A.W.
 Db 126 LEESQVAYRGLFLIDPHGMLRQITVNDMPVGRSVEEVRLLEAFQFVEKHEVCPANWK 185 ; APPLICANT: Bhatia, Ajay
 Qy 251 PGSETIPDAGKLK-YFDK 269 ; APPLICANT: Coler, Rhea
 Db 186 KGAPTMKPEPNASVEGYFSK 205 ; APPLICANT: Probst, Peter
 ; US-09-991-496-97 ; US-09-991-496-97
 Query Match 41.5%; Score 598; DB 9; Length 1427;
 Best Local Similarity 54.0%; Pred. No. 3. 1e-52;
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;
 Qy 72 HSLHLSKAKISKPAPWEGAVI-DGEFKELKLTDYRGKYLVFFYPLDITFVCPEVIA 130 ; APPLICANT: Coler, Rhea
 Db 6 HMSCGNAKINSPPAPSFEEVALMPNGSKKISLSSYKGKWNVVLFFYPLDITFVCPEVIA 65 ; APPLICANT: Probst, Peter
 Qy 131 FGDRLEFRSNTTEVACVSQVSQFTLAWIWPRLGGSPTRILPSLTHQISKDYGV 190 ; APPLICANT: Webb, John R.
 Db 66 FSPSVSRFNLNECVLACSIDSBYAHQLQWTLQDRKKGGGLGTMIAIPMLADKTSIARSYGV 125 ; APPLICANT: Dillon, Devin C.
 Qy 191 YLEDSGHTLRGLIPIDDKGILRQITLNDLPLVGRSYDETRLVQAFQYTDKHEVCPAGWK 250 ; APPLICANT: Skeiky, Yasir A.W.
 Db 126 LEESQVAYRGLFLIDPHGMLRQITVNDMPVGRSVEEVRLLEAFQFVEKHEVCPANWK 185 ; APPLICANT: Bhatia, Ajay
 Qy 251 PGSETIPDAGKLK-YFDK 269 ; APPLICANT: Coler, Rhea
 Db 186 KGAPTMKPEPNASVEGYFSK 205 ; APPLICANT: Probst, Peter
 ; US-09-991-496-97 ; US-09-991-496-97
 Query Match 41.5%; Score 598; DB 9; Length 1641;
 Best Local Similarity 54.0%; Pred. No. 3. 8e-52; Mismatches 51; Indels 2; Gaps 2;
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;
 Qy 97 Application US/09991496 ; APPLICANT: Coler, Rhea
 ; Sequence 97, Application US/09991496 ; APPLICANT: Probst, Peter
 ; Patent No. US20020169285A1 ; APPLICANT: Brannon, Mark
 ; GENERAL INFORMATION: ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; APPLICANT: Reed, Steven G. ; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; APPLICANT: Campos-Neto, Antonio ; FILE REFERENCE: 210121.420C8
 ; APPLICANT: Webb, John R. ; CURRENT APPLICATION NUMBER: US/09/874, 923
 ; APPLICANT: Dillon, Devin C. ; CURRENT FILING DATE: 2001-06-04
 ; APPLICANT: Skeiky, Yasir A.W. ; NUMBER OF SEQ ID NOS: 122
 ; APPLICANT: Bhatia, Ajay ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 97 ; SEQ ID NO 97
 ; LENGTH: 1641 ; LENGTH: 1641
 ; TYPE: PRT ; TYPE: PRT
 ; ORGANISM: Artificial Sequence ; ORGANISM: Artificial Sequence
 ; FEATURE: OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple ; FEATURE: OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; OTHER INFORMATION: Leishmania antigens ; OTHER INFORMATION: Leishmania antigens
 ; US-09-991-496-96 ; US-09-991-496-96
 Query Match 41.5%; Score 598; DB 9; Length 1641;
 Best Local Similarity 54.0%; Pred. No. 3. 8e-52; Mismatches 51; Indels 2; Gaps 2;
 Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

QY 72 HSLHLSKAKTSKPKDYGEGTAVI-DGEFEKELKLTDYRGKYLVFFYPLDTEVCPTETIA 130
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 6 HHMSCGNNAKINSPARSFEEVVALMPNGSFKKLSSYKGKAVVLFYPLDFTVCPTETIA 65

QY 131 FGDRLEEFKSFNTTEVACSTSDQFHLMWINTPROGGIIPRLPLSDLTHQSKDGY 190
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 66 FSDSVSRFNLNECEVLACSIDSEYAHLOWTLDKRGKGTMAPMLADKTKS1TARSYGV 125

QY 191 YLEDSGHTLRLGLFIIDKGKIRQTLNDLPGRSVDETLRLVQAFQYTDKHEVCPAGWK 250
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 126 LEESQGVAYKGLFIDPHGMURTYNDMEYGRSYEEVIRLLEAQFVEKHGEVCPANW 185

QY 251 PGSETTIPDAGKLK-YFDK 269
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 186 KGAPTMKPEPNASVEGYFSK 205

RESULT 15
 US-09-874-923-96
 ; Sequence 96, Application US/09874923
 ; Patent No. US20020081320A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven G.
 ; APPLICANT: Campos-Neto, Antonio
 ; APPLICANT: Webb, John R.
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Coler, Rhea
 ; APPLICANT: Probst, Peter
 ; APPLICANT: Brannon, Mark
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 ; FILE REFERENCE: 210121.420CB
 ; CURRENT APPLICATION NUMBER: US/09/874, 923
 ; CURRENT FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 96
 ; LENGTH: 1641
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; US-09-874-923-96

Query Match 41.5%; Score 598; DB 10; Length 1641;
 Best Local Similarity 54.0%; Pred. No. 3. 8e-52; 2;
 Matches 108; Conservative 39; Mismatches 51; Gaps 2;
 ; Indels 2;

QY 72 HSLHLSKAKTSKPKDYGEGTAVI-DGEFEKELKLTDYRGKYLVFFYPLDTEVCPTETIA 130
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 6 HHMSCGNNAKINSPARSFEEVVALMPNGSFKKLSSYKGKAVVLFYPLDFTVCPTETIA 65

QY 131 FGDRLEEFKSFNTTEVACSTSDQFHLMWINTPROGGIIPRLPLSDLTHQSKDGY 190
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 66 FSDSVSRFNLNECEVLACSIDSEYAHLOWTLDKRGKGTMAPMLADKTKS1TARSYGV 125

QY 191 YLEDSGHTLRLGLFIIDKGKIRQTLNDLPGRSVDETLRLVQAFQYTDKHEVCPAGWK 250
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 126 LEESQGVAYKGLFIDPHGMURTYNDMEYGRSYEEVIRLLEAQFVEKHGEVCPANW 185

QY 251 PGSETTIPDAGKLK-YFDK 269
 | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : ||
 Db 186 KGAPTMKPEPNASVEGYFSK 205

Search completed: January 17, 2003, 19:20:23

Job time : 18 secs

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Maximum DB seq length:	200000000																																																																																																																																																																																				
Post-processing:	Minimum Match 0%																																																																																																																																																																																				
Database :	Maximum Match 100% Listing first 45 summaries																																																																																																																																																																																				
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES																																																																																																																																																																																				
<table border="1"> <thead> <tr> <th>Result No.</th> <th>Score</th> <th>Query Match</th> <th>Length</th> <th>DB ID</th> <th>Description</th> </tr> </thead> <tbody> <tr> <td>1</td> <td>1441</td> <td>100.0</td> <td>271</td> <td>2 G01790</td> <td>probable thiol-specific thiol-specific antithioredoxin</td> </tr> <tr> <td>2</td> <td>744</td> <td>51.6</td> <td>198</td> <td>2 A57716</td> <td>probable thioredoxin</td> </tr> <tr> <td>3</td> <td>740</td> <td>51.4</td> <td>198</td> <td>1 168897</td> <td>probable thioredoxin</td> </tr> <tr> <td>4</td> <td>735</td> <td>51.0</td> <td>199</td> <td>2 A46711</td> <td>probable thioredoxin</td> </tr> <tr> <td>5</td> <td>731</td> <td>50.8</td> <td>200</td> <td>2 151016</td> <td>probable thioredoxin</td> </tr> <tr> <td>6</td> <td>730</td> <td>50.7</td> <td>199</td> <td>2 152425</td> <td>probable thioredoxin</td> </tr> <tr> <td>7</td> <td>721</td> <td>50.1</td> <td>199</td> <td>2 A48513</td> <td>probable thioredoxin</td> </tr> <tr> <td>8</td> <td>701</td> <td>48.6</td> <td>576</td> <td>2 T16005</td> <td>hypothetical protein</td> </tr> <tr> <td>9</td> <td>689</td> <td>47.8</td> <td>257</td> <td>2 JQ0064</td> <td>MERS protein - mouse</td> </tr> <tr> <td>10</td> <td>680</td> <td>47.2</td> <td>195</td> <td>2 JQ2258</td> <td>substrate protein</td> </tr> <tr> <td>11</td> <td>639</td> <td>44.4</td> <td>226</td> <td>2 S43598</td> <td>mer5 homolog R07E5</td> </tr> <tr> <td>12</td> <td>634</td> <td>44.0</td> <td>192</td> <td>2 T41413</td> <td>thioredoxin peroxidase</td> </tr> <tr> <td>13</td> <td>588</td> <td>40.8</td> <td>203</td> <td>2 A12385</td> <td>thioredoxin peroxidase</td> </tr> <tr> <td>14</td> <td>588</td> <td>40.8</td> <td>210</td> <td>2 T05318</td> <td>thiol-specific antioxidant</td> </tr> <tr> <td>15</td> <td>584</td> <td>40.5</td> <td>196</td> <td>2 A47362</td> <td>thiol-specific antioxidant</td> </tr> <tr> <td>16</td> <td>582</td> <td>40.4</td> <td>265</td> <td>2 T09211</td> <td>basal protein - sp1</td> </tr> <tr> <td>17</td> <td>570</td> <td>39.6</td> <td>200</td> <td>2 S76284</td> <td>hypothetical protein</td> </tr> <tr> <td>18</td> <td>568</td> <td>39.5</td> <td>242</td> <td>2 A49173</td> <td>hypothetical protein</td> </tr> <tr> <td>19</td> <td>567</td> <td>39.3</td> <td>196</td> <td>2 S69732</td> <td>hypothetical protein</td> </tr> <tr> <td>20</td> <td>548</td> <td>38.0</td> <td>199</td> <td>2 S73193</td> <td>hypothetical protein</td> </tr> <tr> <td>21</td> <td>479</td> <td>33.3</td> <td>233</td> <td>2 S67947</td> <td>alkyl hydroperoxidase</td> </tr> <tr> <td>22</td> <td>477</td> <td>33.1</td> <td>178</td> <td>2 S29119</td> <td>hypothetical protein</td> </tr> <tr> <td>23</td> <td>477</td> <td>33.1</td> <td>200</td> <td>2 A71689</td> <td>thioredoxin peroxidase</td> </tr> <tr> <td>24</td> <td>474</td> <td>32.9</td> <td>199</td> <td>2 F83540</td> <td>probable alkyl hydroperoxidase</td> </tr> <tr> <td>25</td> <td>474</td> <td>32.9</td> <td>273</td> <td>2 A43862</td> <td>thioredoxin peroxidase</td> </tr> <tr> <td>26</td> <td>467</td> <td>32.4</td> <td>202</td> <td>2 C97756</td> <td>thioredoxin peroxidase</td> </tr> <tr> <td>27</td> <td>461</td> <td>32.0</td> <td>200</td> <td>2 G83204</td> <td>probable peroxidase</td> </tr> <tr> <td>28</td> <td>455</td> <td>31.6</td> <td>195</td> <td>2 G71492</td> <td>probable thioredoxin peroxidase</td> </tr> <tr> <td>29</td> <td>451.5</td> <td>31.3</td> <td>200</td> <td>2 AB0552</td> <td>probable peroxidase</td> </tr> </tbody> </table>	Result No.	Score	Query Match	Length	DB ID	Description	1	1441	100.0	271	2 G01790	probable thiol-specific thiol-specific antithioredoxin	2	744	51.6	198	2 A57716	probable thioredoxin	3	740	51.4	198	1 168897	probable thioredoxin	4	735	51.0	199	2 A46711	probable thioredoxin	5	731	50.8	200	2 151016	probable thioredoxin	6	730	50.7	199	2 152425	probable thioredoxin	7	721	50.1	199	2 A48513	probable thioredoxin	8	701	48.6	576	2 T16005	hypothetical protein	9	689	47.8	257	2 JQ0064	MERS protein - mouse	10	680	47.2	195	2 JQ2258	substrate protein	11	639	44.4	226	2 S43598	mer5 homolog R07E5	12	634	44.0	192	2 T41413	thioredoxin peroxidase	13	588	40.8	203	2 A12385	thioredoxin peroxidase	14	588	40.8	210	2 T05318	thiol-specific antioxidant	15	584	40.5	196	2 A47362	thiol-specific antioxidant	16	582	40.4	265	2 T09211	basal protein - sp1	17	570	39.6	200	2 S76284	hypothetical protein	18	568	39.5	242	2 A49173	hypothetical protein	19	567	39.3	196	2 S69732	hypothetical protein	20	548	38.0	199	2 S73193	hypothetical protein	21	479	33.3	233	2 S67947	alkyl hydroperoxidase	22	477	33.1	178	2 S29119	hypothetical protein	23	477	33.1	200	2 A71689	thioredoxin peroxidase	24	474	32.9	199	2 F83540	probable alkyl hydroperoxidase	25	474	32.9	273	2 A43862	thioredoxin peroxidase	26	467	32.4	202	2 C97756	thioredoxin peroxidase	27	461	32.0	200	2 G83204	probable peroxidase	28	455	31.6	195	2 G71492	probable thioredoxin peroxidase	29	451.5	31.3	200	2 AB0552	probable peroxidase	ALIGMENTS
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RESULT 1	G01790 probable thiol-specific reductase (EC 1.17.1.2) AOE37-2 - human																																																																																																																																																																																				
Qy	1 MEALPLAATTDPDHRRRLPLPLFLPLPAGAVQWETEERPRTRFECHYAGSOV 60																																																																																																																																																																																				
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Qy	61 PGEASRVSDAHSUHLSKAKISKAPKAPYWGATVIGERKELKLTDYRGKYLFFFPYLD 120																																																																																																																																																																																				
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Qy	121 TFCVCPTEITAFGDRLEEFFSINTEVACSVSDOFTHLAWINTPRQGGIGPIRPLSL 180																																																																																																																																																																																				
Db	121 TFCVCPTEITAFGDRLEEFFSINTEVACSVSDQFTHLAWINTRRQGGIGPIRPLSL 180																																																																																																																																																																																				
Qy	181 THOISKDYQVYLESGHTGFLTIDKGILROITLNDLPGVGSVDETLRLVQAFQYD 240																																																																																																																																																																																				
Db	181 THOISKDYQVYLESGHTGFLTIDKGILROITLNDLPGVGSVDETLRLVQAFQYD 240																																																																																																																																																																																				
Qy	241 HGEVCPAGKWPGSTETIPDAGKLKYFDLN 271																																																																																																																																																																																				
Db	241 HGEVCPAGKWPGSTETIPDAGKLKYFDLN 271																																																																																																																																																																																				
RESULT 2	A57716 thiol-specific antioxidant - rat																																																																																																																																																																																				
C;Species:	Rattus norvegicus (Norway rat)																																																																																																																																																																																				
C;Date:	23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jun-1999																																																																																																																																																																																				
C;Accession:	A57716																																																																																																																																																																																				
R;Chae, H.Z.; Robison, K.; Poole, L.B.; Church, G.; Storz, G.; Rhee, S.G.	Proc. Natl. Acad. Sci. U.S.A. 91, 7017-7021, 1994																																																																																																																																																																																				

A;Title: Cloning and sequencing of thiol-specific antioxidant from mammalian brain: alkyl hydroperoxide reductase, C15-156; MUID:94316629; PMID:8041738

A;Accession: A57716

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-198 <CHA>

A;Cross-references: GB:J06099; NID:9514253; PID:AAA19959_1; PID:9514254

C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 protein

F;15-156/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match Similarity 51.6%; Score 744; DB 2; Length 198; Matches 137; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

Qy 79 AKISKPAPYWEQTAVIDGKFELKLTDYRGKLYVFFYPLDFTFVCPTEIAFGRL 138

Db 6 AHICKPAPDPFTGTAVIDGAFKEIKRLSDYRGKLYVFLFYPPLDFTFVCPTEIAFSDHAEF 65

Qy 139 RSINTEVVACSVQSSQFTLHAWINPPIRGGLGPIRPLSLDTHQISDYGVLWESHT 198

Db 66 RKLGCEVGLGVSDQFNHLAWINPPIRGKLYVFLFYPPLDFTFVCPTEIAFSDHAEF 65

Qy 199 LRGIFLIDDKGILRQITLNDLPGVRSVDTLRLVQAFQYTDKIGEVCPAGWKGSSETIP 258

Db 126 YRGFLIDDKGILRQITLNDLPGVRSVDTLRLVQAFQYTDKIGEVCPAGWKPGSDTIKP 185

Qy 259 DPAGKLKYFDKLN 271

Db 186 NVDDSKEYFSKHN 198

RESULT 3

18897 probable thioredoxin peroxidase (EC 1.11.1.-) 1 - human

N;Alternate names: enhancer protein; heme-binding 23K protein (HBP23); natural killer cell

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 02-Jun-2000

C;Accession: I68897; I38341

R;Shau, H.; Butterfield, L.H.; Chiu, R.; Kim, A.

Immunogenetics 40, 129-134, 1994

A;Title: Cloning and sequence analysis of candidate human natural killer-enhancing factor

A;Reference number: I54533; MUID:94299283; PMID:8026862

A;Accession: I68897

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-198 <SHA>

A;Cross-references: GB:LL19185; NID:9440307; PIDN:AAA50465_1; PID:9440308

R;Lim, Y.S.; Cha, M.K.; Kim, H.K.; Kim, I.H.

Gene 140, 279-284, 1994

A;Title: The thiol-specific antioxidant protein from human brain: gene cloning and analysis

A;Reference number: I38341; MUID:94193012; PMID:8144038

A;Accession: I38341

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-198 <SHA>

A;Cross-references: EMBL:222548; NID:9438068; PIDN:CAA80269_1; PID:943069; GB:LI4286

A;Note: this sequence has been revised in EMBL:222548 and differs at positions 60-66 from

C;Genetics:

A;Gene: GDB:TPKX1; PRP; NKEFB

A;Cross-references: GDB:594943

A;Map position: 13q11-13q2

C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 protein

F;15-156/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match Similarity 51.0%; Score 735.5; DB 2; Length 199; Matches 135; Conservative 25; Mismatches 31; Indels 1; Gaps 1;

Qy 79 AKISKPAPYWEQTAVIDGKFELKLTDYRGKLYVFFYPLDFTFVCPTEIAFGRL 137

Db 6 AKIKHPAPDPFTGTAVIDGAFKEIKRLSDYRGKLYVFLFYPPLDFTFVCPTEIAFSDHAEF 65

Qy 138 RSINTEVVACSVQSSQFTLHAWINPPIRGGLGPIRPLSLDTHQISDYGVLWESHT 197

Db 66 FKKLNCOVIGASVDSHCHLAWINPPIRGKLYVFLFYPPLDFTFVCPTEIAFSDRAE 125

Qy 198 TURGLFIDDKGILRQITLNDLPGVRSVDTLRLVQAFQYTDKIGEVCPAGWKGSSETI 257

Db 126 SPRGLFIDDKGILRQITLNDLPGVRSVDTLRLVQAFQYTDKIGEVCPAGWKPGSDTIKP 185

Qy 258 DPAGKLKYFDKL 269

Db 186 PDVQSKKEYFSK 197

RESULT 4

A46711 probable thioredoxin peroxidase (EC 1.11.1.-) PAGA - human

N;Alternate names: enhancer protein; heme-binding 23K protein (HBP23); natural killer cell

C;Species: Homo sapiens (man)

C;Accession: A46711; I54533; S32099

R;Prosperi, M.T.; Ferbus, D.; Karczinski, I.; Goubin, G.

J. Biol. Chem. 268, 11050-11056, 1993

A;Title: A human cDNA corresponding to a gene overexpressed during cell proliferation

A;Reference number: A46711; MUID:93266552; PMID:849166

A;Molecule type: mRNA

A;Residues: 1-199 <PRO>

A;Cross-references: EMBL:x67951; NID:9278640; PIDN:CAA48137_1; PID:9287641

A;Experimental source: rat-transformed mammary epithelial cell line HBL100

A;Note: sequence extracted from NCBI backbone (NCBI:132000)

R;Shau, H.; Butterfield, L.H.; Chiu, R.; Kim, A.

Immunogenetics 40, 129-134, 1994

A;Title: Cloning and sequence analysis of candidate human natural killer-enhancing factor

A;Reference number: I54533; MUID:94299283; PMID:8026862

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-198 <CC> 151-188, 'P', 190, 'T', 192-199 <SHA>

A;Cross-references: GB:LL19184; NID:9440305; PIDN:AAA50464_1; PID:9440306

C;Genetics: \

A;Gene: GDB:TPA

A;Cross-references: GDB:230262; OMIM:176763

A;Map position: 1P34.1-1P34.1

C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 protein

F;15-157/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match Similarity 50.0%; Score 735.5; DB 2; Length 198; Matches 135; Conservative 25; Mismatches 31; Indels 1; Gaps 1;

Qy 79 AKISKPAPYWEQTAVIDGKFELKLTDYRGKLYVFFYPLDFTFVCPTEIAFGRL 137

Db 6 AKIKHPAPDPFTGTAVIDGAFKEIKRLSDYRGKLYVFLFYPPLDFTFVCPTEIAFSDHAEF 65

Qy 138 RSINTEVVACSVQSSQFTLHAWINPPIRGGLGPIRPLSLDTHQISDYGVLWESHT 197

Db 66 FKKLNCOVIGASVDSHCHLAWINPPIRGKLYVFLFYPPLDFTFVCPTEIAFSDRAE 125

Qy 198 TURGLFIDDKGILRQITLNDLPGVRSVDTLRLVQAFQYTDKIGEVCPAGWKGSSETI 257

Db 126 SPRGLFIDDKGILRQITLNDLPGVRSVDTLRLVQAFQYTDKIGEVCPAGWKPGSDTIKP 185

Qy 258 DPAGKLKYFDKL 269

Db 186 PDVQSKKEYFSK 197

RESULT 5

15106 proliferation associated protein pag homolog, 25K - Japanese common newt

C;Species: Cynops pyrhogaster (Japanese common newt)

C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 19-May-2000

RESULT 12	
T41413	thioredoxin peroxidase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe	C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C;Accession: T41413; T50561	R;Wood, V.; Reilandram, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
A;Accession: T41413; 221954	submitted to the EMBL Data Library, September 1998
A;Accession: T41413	A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA	A;Description: thioredoxin peroxidase from Schizosaccharomyces pombe.
A;Residues: 1-192 <NOD>	A;Reference number: z25073
A;Cross-references: EMBL:AL031798; PIDN:CAA21182.1; GSPDB:GN00068; SPDB:SPCC576.03c	A;Cross-references: strain 972h(-); cosmid c576
A;Experimental source: R;Koo, K.H.; Kim, K.; Chae, H.Z.	A;Submitted to the EMBL Data Library, August 1998
A;Gene: R;Koo, K.H.; Kim, K.; Chae, H.Z.	A;Description: thioredoxin peroxidase from Schizosaccharomyces pombe.
A;Molecule type: mRNA	A;Accession: T50461
A;Status: preliminary; translated from GB/EMBL/DDJB	A;Status: preliminary; translated from GB/EMBL/DDJB
A;Residues: 1-192 <NOD>	A;Residues: 1-192 <NOD>
A;Cross-references: EMBL:AF083335; PIDN: AAC71013.1	A;Cross-references: EMBL:AF083335; PIDN: AAC71013.1
A;Gene: SPDB:SPCC576.03c	A;Gene: SPDB:SPCC576.03c
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein	C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein
Query Match	Query Match
Best Local Similarity 60.0%; Pred. No. 9.6e-51; Matches 114; Conservative 36; Mismatches 38; Indels 2; Gaps 1;	Best Local Similarity 44.0%; Score 634; DB 2; Length 192; Matches 114; Conservative 36; Mismatches 38; Indels 2; Gaps 1;
Db 80 KISKPPAPYWEGTAVIDGEFFBLKLTDYRGKYLVFFYPLDFTFWCPTEITAFGDRLEEFF 139	Db 80 KISKPPAPYWEGTAVIDGEFFBLKLTDYRGKYLVFFYPLDFTFWCPTEITAFGDRLEEFF 139
Qy 140 SINTENVACSVDSQFTHLAWINTPRQGGGLPIRPLSLDTHQSKDGYVLEDSGHT 199	Qy 140 SINTENVACSVDSQFTHLAWINTPRQGGGLPIRPLSLDTHQSKDGYVLEDSGHT 199
Db 64 ERNAQVILTSTDSEYSHLAFINTPRKEGGGINPLADPSHKVSRDYGVLIEDAGVA 123	Db 64 ERNAQVILTSTDSEYSHLAFINTPRKEGGGINPLADPSHKVSRDYGVLIEDAGVA 123
Qy 200 RGLFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHEGVCPAGKPGSETIIPD 259	Qy 200 RGLFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHEGVCPAGKPGSETIIPD 259
Db 124 RGLFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHEGVCPAGKPGSETIIPD 181	Db 124 RGLFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHEGVCPAGKPGSETIIPD 181
Qy 260 PAGKLKYFDK 269	Qy 260 PAGKLKYFDK 269
Db 182 TKNPKYFSK 191	Db 182 TKNPKYFSK 191
RESULT 13	
A12385	peroxiredoxin [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.	C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120	C;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002	C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: A12385	C;Accession: A12385
R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, N.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S	R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, N.; Nakazaki, N.; Shimojo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana	A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MID:21595285; PMID:11759840	A;Reference number: AB1807; MID:21595285; PMID:11759840
A;Accession: A12385	A;Accession: A12385
A;Status: preliminary	A;Status: preliminary
A;Molecule type: DNA	A;Molecule type: DNA
A;Residues: 1-203 <NUR>	A;Residues: 1-203 <NUR>
A;Cross-references: GB:BA00019; PIDN:BA076340.1; PID:917133778; GSPDB:GN00179	A;Cross-references: strain PCC 7120
A;Experimental source: C;Genetics:	A;Experimental source: C;Genetics:
A;Gene: alr4641	A;Gene: alr4641
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein	C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein
RESULT 14	
T06318	thiol-specific antioxidant protein precursor homolog TSA - wheat (fragment)
C;Species: Triticum aestivum (common wheat)	C;Species: Triticum aestivum (common wheat)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000	C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06318	C;Accession: T06318
R;Tsunoyama, T.	R;Tsunoyama, T.
A;Status: submitted to the EMBL Data Library, January 1997	A;Status: submitted to the EMBL Data Library, January 1997
A;Reference number: T21590	A;Reference number: T21590
A;Accession: T06318	A;Accession: T06318
A;Molecule type: mRNA	A;Molecule type: mRNA
A;Residues: 1-210 <TSU>	A;Residues: 1-210 <TSU>
A;Cross-references: EMBL:AB000405; PIDN:BAA19099.1	A;Cross-references: EMBL:AB000405; PIDN:BAA19099.1
A;Experimental source: cv. Norin-no 61, seedlings	A;Experimental source: cv. Norin-no 61, seedlings
A;Genetics: C	A;Genetics: C
A;Gene: TSA	A;Gene: TSA
A;Genome: nuclear	A;Genome: nuclear
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein	C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein
C;Keywords: chloroplast	C;Keywords: chloroplast
F;1-3D/Domain: transit peptide (chloroplast) (fragment) #status Predicted <TNP>	F;1-3D/Domain: transit peptide (chloroplast) (fragment) #status Predicted <TNP>
F;27-169/Domain: alkyl hydroperoxidase C22 protein homology <C22> #status Predicted <MAT>	F;27-169/Domain: alkyl hydroperoxidase C22 protein homology <C22> #status Predicted <MAT>
F;31-210/Product: thiol-specific antioxidant protein homolog #status Predicted <MAT>	F;31-210/Product: thiol-specific antioxidant protein homolog #status Predicted <MAT>
Query Match	Query Match
Best Local Similarity 40.8%; Score 588.5; DB 2; Length 210; Matches 111; Conservative 33; Mismatches 52; Indels 5; Gaps 2;	Best Local Similarity 40.8%; Score 588.5; DB 2; Length 210; Matches 111; Conservative 33; Mismatches 52; Indels 5; Gaps 2;
Db 11 AAAEYDPL---VGKNAKPDPFAAEVFDQEFINVKLSLQDYGKVVLFYPLDFTFWCP 66	Db 11 AAAEYDPL---VGKNAKPDPFAAEVFDQEFINVKLSLQDYGKVVLFYPLDFTFWCP 66
Qy 68 SVADHSILSKAKISKPPAPYWEGTAVIDGEFFBLKLTDYRG-KYLVFFYPLDFTFWCP 126	Qy 68 SVADHSILSKAKISKPPAPYWEGTAVIDGEFFBLKLTDYRG-KYLVFFYPLDFTFWCP 126
Db 127 EIIAFSDRLEFRSINTENVACSVDSQFTHLAWINTPRQGGGLPIRPLSLDTHQISK 186	Db 127 EIIAFSDRLEFRSINTENVACSVDSQFTHLAWINTPRQGGGLPIRPLSLDTHQISK 186
Db 67 ETIATSDRHEEKFINTELIGVSVSFHAWTVERKSGGLGKLYPLVSDFVHSISK 126	Db 67 ETIATSDRHEEKFINTELIGVSVSFHAWTVERKSGGLGKLYPLVSDFVHSISK 126
Qy 187 DGYVVDLSDGHSMLRGKFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHE 246	Qy 187 DGYVVDLSDGHSMLRGKFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHE 246
Db 127 SFGVLIPDQGTLRGKFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHE 186	Db 127 SFGVLIPDQGTLRGKFLIDDKILRQTLNDLPGVRSVDETRLQVAFQYDNGKHE 186
Qy 247 AGWKPGSETIIPDPAKLYF 267	Qy 247 AGWKPGSETIIPDPAKLYF 267
Db 187 AGWKPGSEKSMKPDKPGSKKEYF 207	Db 187 AGWKPGSEKSMKPDKPGSKKEYF 207
RESULT 15	
A47362	thiol-specific antioxidant - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YML028W	N;Alternate names: protein YML028W
C;Species: Saccharomyces cerevisiae	C;Species: Saccharomyces cerevisiae
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999	C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999

C;Accession: A47362; B47362; S49751;
 R;Chae, H. Z.; Kim, I. H.; Kim, K.; Rhee, S. G.
 J. Biol. Chem. 268, 16815-16821, 1993
 A;Title: Cloning, sequencing, and mutation of thiol-specific antioxidant gene of *Saccharomyces cerevisiae*
 A;Reference number: A47362; MUID:93346439; PMID:8344960
 A;Accession: A47362
 A;Molecule type: DNA
 A;Residues: 1-196 <CH2>
 A;Cross-references: EMBL:Z46559; NID:9575680; PIDN:CAA86627_1; PID:9575691
 A;Note: sequence extracted from NCBI backbone (NCBIN:135846, NCBI:135847)
 A;Accession: B47362
 A;Molecule type: protein
 A;Residues: 2-13; 62-68; 79-87; 90-94; 137-143; 148-153; 155-160; 192-196 <CH2>
 A;Genetics:
 A;Gene: SGD:TSAL
 A;Cross-references: SGD:S0004490; MIPS:YML028w
 A;Map position: 13L
 C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein
 C;Keywords: transmembrane protein
 F;2-196/Product: thiol specific antioxidant #status experimental <MAT>
 F;12-153/Domain: alkyl hydroperoxidase c22 protein homology <c22>
 F;34-50/Domain: transmembrane #status predicted <TM>

Query Match
 Best local similarity 55.4%; Score 584; DB 2; Length 196;
 Matches 107; Conservative 33; Mismatches 53; Indels 0; Gaps 0;

QY 79 AKISKPAPWEGPAVIDEEFKELKLTDYRGKIVWFFFVPLDFWVCPPEIAFGDRLEEF 138
 |:|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 3 AQQKQOQAPTFKKKAVDGFDEVSIDKKKGKVYVLAFTPLAFVCPPEIAFGDRLEEF 62
 QY 139 RSINTEVACSVSDQFTHLAWIITPRQGLGPRIPLSLDTHQISKDYGVYLEDGHT 198
 |:|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 63 EEQGAQVLFASTDSEYSLLAWINNPRKEGGIPLNIPLADRNHSLRDYGVVLEEGVA 122
 QY 199 LRGFLIIDKGIIQITNDLPVGRSYDTETRLVQAFQYTDKIGEVOPAGWIPGSETIP 258
 |:|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 123 LRGFLIIDPKGVIRHITINDLPVGRNVDEALRIVAFQWTDKNGTVLPCNNWTPGAATKP 182
 QY 259 DPAGKLYFDKLN 271
 Db 183 TVERDSKEYFEAAN 195

Search completed: January 17, 2003, 19:19:37
 Job time : 24 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model.
Run on: January 17, 2003, 19:15:03 ; Search time 39 Seconds

(without alignments)
925.921 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441
Sequence: 1 MEALPLLAATTTPDHGRHRRLL.....GSETTIPDPAGKLYFDKLN 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1986.DAT:*

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11: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1992.DAT:*

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21: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2002.DAT:*

RESULT 1		ALIGNMENTS	
ID	AAW12692	ID	AAW12692 standard; Protein; 271 AA.
XX		XX	
AC	AAW12692;	AC	
XX		XX	
DT	05-SEP-1997 (first entry)	DT	
XX		XX	
DE	Natural killer cell enhancing factor C.	DE	
XX		XX	
Natural killer cell enhancing factor C; NKEF C; human; leukaemia cell; natural killer cell; lymphocyte; tumour cell; superoxide radical; LAK; lymphokine-activated killer cell; interleukin-2; growth inhibition; enhanced cell proliferation; antioxidant; vasoactive stromatitis virus; inhibitor; viral infection; inflammation; neoplasia; therapy.	Natural killer cell enhancing factor C; NKEF C; human; leukaemia cell; natural killer cell; lymphocyte; tumour cell; superoxide radical; LAK; lymphokine-activated killer cell; interleukin-2; growth inhibition; enhanced cell proliferation; antioxidant; vasoactive stromatitis virus; inhibitor; viral infection; inflammation; neoplasia; therapy.	Natural killer cell enhancing factor C; NKEF C; human; leukaemia cell; natural killer cell; lymphocyte; tumour cell; superoxide radical; LAK; lymphokine-activated killer cell; interleukin-2; growth inhibition; enhanced cell proliferation; antioxidant; vasoactive stromatitis virus; inhibitor; viral infection; inflammation; neoplasia; therapy.	
KW		KW	
KW		KW	
KW		KW	
OS	Home sapiens.	OS	
XX		XX	
PN	W09639424-A1.	PN	
XX		XX	
PD	12-DEC-1996.	PD	
XX		XX	
PF	06-JUN-1995;	PF	06-JUN-1995; 95W0-US07200.
XX		XX	
PR	06-JUN-1995;	PR	06-JUN-1995; 95W0-US07200.
XX		XX	
PA	(HUMA-) HUMAN GENOME SCI INC.	PA	
XX		XX	
PI	Gentz R, Ni J, Rosen CA, Yu G;	PI	
XX		XX	
DR	WPI: 1997-043059/04.	DR	
XX		XX	
N-PSDB; AAT51788.	N-PSDB; AAT51788.		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1441	100.0	271	18 AAW12692	Natural killer cell
2	1441	100.0	271	21 AAY43399	Human natural killer
3	1441	100.0	271	22 AAM50249	Human natural killer
4	1441	100.0	271	22 AAB82478	Natural killer cell
5	1441	100.0	271	22 AAB8038	Amino acid sequenc
6	854	59.3	242	22 AAB58323	Drosophila melanog
7	750	52.1	233	21 AAB43528	Human cancer assoc
8	750	52.1	233	23 ABP11353	Human ovarian anti
9	746	51.8	198	22 AAB8036	Amino acid sequenc
10	721	50.0	198	22 AAB68040	Amino acid sequenc

PT DNA encoding human natural killer cell enhancing factor C - useful
PT for preventing or treating viral infections, inflammation, neoplasia
PT and damage from superoxide radicals
XX

PS Claim 1; Fig 1; 61pp; English.

CC This sequence represents the human natural killer cell enhancing factor
CC of NK (NKEF) C. Natural killer cells (NK) are a subset of lymphocytes capable
CC of lysing a variety of tumour cells without prior activation.
CC Lymphokine-activated killer cells (LAK) are mainly NK cells activated by
CC interleukin-2, and are capable of lysing wider ranges of tumour cells
CC with higher cytotoxic activity. NK/LAK activity is influenced by various
CC components of blood, including the NKEF A and B proteins. Transfection of
CC NKEF into cells results in cell-type-dependent enhanced cell
CC proliferation or growth inhibition. The NKEF proteins are antioxidants,
CC but show no sequence homology to other antioxidants, such as catalase or
CC superoxide dismutase. This sequence, or the DNA encoding it can be used
CC to inhibit the cytopathic effect of vesicular stomatitis virus and to
CC inhibit the growth of leukaemia cells, or to treat a patient in need of a
CC NKEF C polypeptide. Disease or a susceptibility to disease related to an
CC under-expression of this protein can be diagnosed by determining a
CC mutation in the DNA encoding this sequence. This protein can also be used
CC to identify compounds which bind to and activate a receptor for it. The
CC products can also be used to treat viral infections, inflammation,
CC neoplasia and damage from superoxide radicals.

SQ Sequence 271 AA;

Query Match 100 %; Score 1441; DB 18; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.4e-147; Mismatches 0; Indels 0; Gaps 0;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPILAAATPDHGRHRRRLPLPLFLPLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 120
1 MEALPILAAATPDHGRHRRRLPLPLFLPLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 60

QY 61 PGESRVSVAHDHSLSKAKSKPAPYWGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 120
1 PGESRVSVAHDHSLSKAKSKPAPYWGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 60

Db 61 PGESRVSVAHDHSLSKAKSKPAPYWGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 120
1 PGESRVSVAHDHSLSKAKSKPAPYWGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 60

QY 121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDQFTHLAWINTPRROGGLGPIRPLSDL 180
121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDQFTHLAWINTPRROGGLGPIRPLSDL 180

Db 181 THQISKDGYVYLEDSHGLTGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240
181 THQISKDGYVYLEDSHGLTGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240

QY 241 HGEVCPAGWKPGSEETIPDPAGKLKYFDKLN 271
Db 241 HGEVCPAGWKPGSEETIPDPAGKLKYFDKLN 271

RESULT 2

QY AAY43399 standard; Protein: 271 AA.
ID AAY43399
AC AAY43399;
XX
DT 28-JAN-2000 (first entry)

DE Human natural killer cell enhancing factor C protein sequence.

XX Natural killer cell enhancing factor C; NKEF C; human; diagnosis; probe;
KW viral infection; inflammation; neoplasia; superoxide radical damage;
KW bone marrow rejection; therapy.
OS Homo sapiens.

XX
PN US5995612-A.
XX
PD 16-NOV-1999.

PF 06-JUN-1995; 95US-0467265.
PT XX
PR 06-JUN-1995; 95US-0467265.
XX
PA (YUGG/) YU G.
PA (GENTZ/) GENTZ R.
PA (ROSEN/) ROSEN C A.
PA (NIJJ/) NI J.
XX
PI Gentz R, Rosen CA, Yu G, Ni J;
XX
DR WPI: 2000-012791/01.
XX
DR N-PSDB, AR237242.

CC Isolated polynucleotides encoding human natural killer cell enhancing
PT factor C, useful for preventing, diagnosing or treating viral
PT infections, neoplasia and damage from superoxide radicals -
XX

PS Claim 1; Fig 1; 29pp; English.

CC This sequence is the human natural killer cell enhancing factor C
CC (NKEF C) of the invention. NKEF C protein and DNA sequences can be used
CC in the diagnosis, prevention, and treatment of disorders associated with
CC inappropriate expression and activity (normally reduced) of NKEF C and to
CC augment the action of natural killer cells and proteins. The NKEF C
CC sequences may be used to treat disorders such as viral infections,
CC inflammation, neoplasias and damage from superoxide radicals. They may be
CC administered to treat the above diseases by rectifying mutations or
CC deletions in a patient's genome that affect the activity of NKEF C by
CC expressing inactive proteins or to supplement the patient's own production
CC of NKEF C. Antisense nucleic acid molecules may be administered to down
CC regulate NKEF C expression by binding with the cell's own NKEF C genes and
CC preventing their expression. The NKEF C DNA and antisense molecules may
CC also be used as probe in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acid sequences in samples, and hence which
CC patients may be in need of restorative therapy. They may also be used to
CC study the expression and function of NKEF C and its role in metabolism.
CC NKEF C fragments may be used as antigens in the production of antibodies
CC against NKEF C and in assays to identify modulators (agonists and
CC antagonists) of NKEF C expression and activity. Anti-NKEF C antibodies
CC and NKEF C antagonists may also be used to down regulate NKEF C
CC expression and activity. They may also be used in this way to treat disorders
CC such as the treatment of bone marrow rejection. The antibodies may also
CC be used as diagnostic reagents for identifying the presence of NKEF C in
CC samples.
XX
SQ Sequence 271 AA;

Query Match 100 %; Score 1441; DB 21; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.4e-147; Mismatches 0; Indels 0; Gaps 0;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEALPILAAATPDHGRHRRRLPLPLFLPLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 120
1 MEALPILAAATPDHGRHRRRLPLPLFLPLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 60

Db 61 PGESRVSVAHDHSLSKAKSKPAPYWGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 120
1 PGESRVSVAHDHSLSKAKSKPAPYWGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 60

QY 121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDQFTHLAWINTPRROGGLGPIRPLSDL 180
121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDQFTHLAWINTPRROGGLGPIRPLSDL 180

Db 181 THQISKDGYVYLEDSHGLTGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240
181 THQISKDGYVYLEDSHGLTGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240

QY 241 HGEVCPAGWKPGSEETIPDPAGKLKYFDKLN 271
Db 241 HGEVCPAGWKPGSEETIPDPAGKLKYFDKLN 271

RESULT 3

ID AAM50249 standard; Protein; 271 AA.

XX

AC AAM50249;

DT 21-JAN-2002 (first entry)

DE Human natural killer cell enhancing factor C.

XX

KW Natural killer cell enhancing factor C; NKEF C; human; antiviral; virucide; antiinflammatory; cyostatic; antioxidant; vulnerable; therapy; diagnosis.

XX

OS Homo sapiens.

XX

PH

Key Peptide 1..30

FT /label= Signal_peptide

FT 31..271

FT /label= Mature_protein

XX

US6294164-B1.

XX

PD 25-SEP-2001.

XX

PF 29-SEP-1999; 99US-0407891.

XX

PR 06-JUN-1995; 95US-0467265.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PT Ni J, Yu G, Gentz R, Rosen CA;

XX

DR WPI; 2001-647258/774.

XX

PT N-PSDB; AAI70524.

XX

PT Natural killer cell enhancing factor C polypeptides encoded by the cDNA in ATCC Deposit No. 97157, useful for preventing or treating viral infections, inflammation, neoplasia or damage from superoxide radicals, e.g. tissue injury

XX

PS Claim 1; Fig 1; 29pp; English.

XX

CC The present sequence is that of human natural killer cell enhancing factor C (NKEF C), as deduced from a cDNA clone (see AAI70524) isolated from a cDNA library derived from cyclohexamide-treated CEM cells. NKEF C is structurally related to highly conserved oxidative stress proteins and shows 68% identity and 83% similarity to NKEF B. NKEF C is highly expressed in heart, liver, skeletal muscle, pancreas, testis and ovary, moderately expressed in placenta, lung, prostate, small intestine and colon, and lowly expressed in brain, spleen, thymus and peripheral blood leucocytes. NKEF C polypeptide is useful for preventing and/or treating viral infections, inflammation, neoplasia or damage from superoxide radicals (e.g. tissue injury or ageing). The polypeptide may also be used for inhibiting the cytopathic effect of vesicular stomatitis virus and for inhibiting the growth of leukaemia cells. The polypeptide and polynucleotide are also useful as research reagents, for constructing DNA vectors, and for developing therapeutics and diagnostics for treating human disease. Polypeptide fragments of NKEF C that have growth inhibitory or antiviral activity are claimed.

XX

SQ Sequence 271 AA;

Query Match 100.0%; Score 1441; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. 1.4e-147; Mismatches 0; Indels 0; Gaps 0;

Matches 271; Conservative 0;

QY 1 MEALPLLAATPDHGRHLRLPLPLFLPAGAVQWETERRPRREECHFYAGQVY 60

DB 1 MEALPLLAATPDHGRHLRLPLPLFLPAGAVQWETERRPRREECHFYAGQVY 60

1 MEALPLLAATPDHGRHLRLPLPLFLPAGAVQWETERRPRREECHFYAGQVY 60

RESULT 4

QY 61 PGEASRVSDAHLHLISKAKISKPAWPWEGTAVIDGEFKEKLKLTDYRGKVLVFFYPLDF 120

Db 61 PGEASRVSDAHLHLISKAKISKPAWPWEGTAVIDGEFKEKLKLTDYRGKVLVFFYPLDF 120

XX

AC RAB82478;

DT 22-AUG-2001 (first entry)

XX

DE Natural killer cell enhancing factor C.

XX

KW Natural killer cell enhancing factor C; NKEF C; human; antioxidant; virucide; antiinflammatory; virucide; antitumour; therapy; diagnosis.

XX

OS Homo sapiens.

XX

PH

Key Peptide 1..30

FT /label= Signal_peptide

FT 31..271

FT /label= Mature_protein

XX

US6255079-B1.

XX

PD 03-JUL-2001.

XX

PF 06-JUN-1995; 95US-0467265.

XX

PR 06-JUN-1995; 95US-0467265.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PT Ni J, Yu G, Gentz R, Rosen CA;

XX

DR WPI; 2001-396982/42.

XX

DR N-PSDB; AAF0573.

XX

PT Isolated polynucleotides encoding human natural killer cell enhancing factor C, useful for preventing, diagnosing or treating viral infections, neoplasia and damage from superoxide radicals

XX

PS Claim 1; Fig 1; 49pp; English.

XX

CC The present sequence is that of human natural killer cell enhancing factor C (NKEF C). NKEF C is highly expressed in heart, liver, skeletal muscle, pancreas, testis and ovary, moderately in placenta, lung, prostate, small intestine and colon, and lowly expressed in brain, spleen, thymus and peripheral blood leucocytes. cDNA (see AAF0573) encoding NKEF C was derived from cyclohexamide-treated CEM cells. The protein shows 83.3% amino acid similarity to NKEF B, and shows significant homology to several other proteins (thiol-specific antioxidants) from a wide range of organisms. The invention provides NKEF C polypeptides, especially a polypeptide comprising amino acids 1-271, or 31-271 of the present sequence, isolated nucleic acids encoding them, and methods

CC of producing the polypeptides in recombinant host cells. The NKEF
 CC C polypeptides and polyuridylates can be used to inhibit the
 CC growth of leukaemia cells, to treat viral infection, to augment the
 CC effects of NK protein, to treat neoplasias such as tumours and
 CC cancers, to prevent inflammation, and to prevent damage from
 CC superoxide radicals in the body e.g. in tissue injury and ageing.
 CC The polypeptides can also be used to screen for potential agonists
 CC and antagonists of NKEF C activity. Antagonists may be useful in
 XX the treatment of bone marrow transplant rejection.

Sequence 271 AA;

Query Match 100.0%; Score 1441; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.4e-147; Mismatches 0; Indels 0; Gaps 0;

Db 1 MEALPLAATPDHGRRHLRLPLFLPAGAVQGWETEERPTREECFHAGGQVY 60

Qy 61 PGEASRVSVADHSIHLSLKAKISKAPWYGMGATVAVIDGEFELKLYDGYLYVFFYPLDF 120

Db 61 PGEASRVSVADHSIHLSLKAKISKAPWYGMGATVAVIDGEFELKLYDGYLYVFFYPLDF 120

Qy 121 TFCVCPTEIIAFGRLEERSINTEWVACSVSDQFTHLAWINTPRQGGLGPIRIPPLSDL 180

Db 121 TFCVCPTEIIAFGRLEERSINTEWVACSVSDQFTHLAWINTPRQGGLGPIRIPPLSDL 180

Qy 181 THQISKDGYVYLEDSGTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFQYTDK 240

Db 181 THQISKDGYVYLEDSGTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFQYTDK 240

Qy 241 HGEVCAGWKPGSETIIPDPAGKLKFDKLN 271

Db 241 HGEVCAGWKPGSETIIPDPAGKLKFDKLN 271

RESULT 5
 AAB69038
 ID AAB69038 standard; peptide; 271 AA.

AC AAB69038;
 XX
 XX
 XX
 DT 29-JUN-2001 (first entry)

DE Amino acid sequence of the acid form of peroxiredoxin TDIXN.
 XX Peroxiredoxin; acid form; oxidative stress; cell death; cancer;
 KW autoimmune disease; neurodegeneration; metabolic disorder.
 OS Homo sapiens.

XX FR2798672-A1.

PN 23-MAR-2001.

PD 17-SEP-1999; 99FR-0011663.

XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PI Rabilloud T;

XX DR WPI; 2001-259869/27.

PT Purified acid form of peroxiredoxin, a marker of oxidative stress,
 PT useful in diagnosis and for identifying potential apoptotic and
 PT anti-apoptotic agents comprises a specific amino acid motif close to
 XX the active site -

XX Claim 12; Page 23-24; 28pp; French.

CC The present sequence represents the acid form of a human peroxiredoxin
 CC enzyme. The acid form of peroxiredoxin is a characteristic marker of
 CC oxidative stress that can be measured simply and quickly, providing a
 CC reliable indication of stress even where this is of short duration.
 CC Modulators of the acid form of peroxiredoxin enzyme are used for the
 CC stimulation or inhibition of apoptosis. Compounds that stimulate
 CC formation of the acid form of peroxiredoxins are used to induce cell
 CC death (treatment of cancer and autoimmune diseases) while those that
 CC inhibit its formation are used to prevent cell death (treatment of
 CC neurodegeneration). Measuring the ratio between acid form and the native
 CC form of peroxiredoxin is used to diagnose metabolic disorders associated
 XX with oxidative stress.

Sequence 271 AA;

Query Match 100.0%; Score 1441; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.4e-147; Mismatches 0; Indels 0; Gaps 0;

Db 1 MEALPLAATPDHGRRHLRLPLFLPAGAVQGWETEERPTREECFHAGGQVY 60

Qy 61 PGEASRVSVADHSIHLSLKAKISKAPWYGMGATVAVIDGEFELKLYDGYLYVFFYPLDF 120

Db 61 PGEASRVSVADHSIHLSLKAKISKAPWYGMGATVAVIDGEFELKLYDGYLYVFFYPLDF 120

Qy 121 TFCVCPTEIIAFGRLEERSINTEWVACSVSDQFTHLAWINTPRQGGLGPIRIPPLSDL 180

Db 121 TFCVCPTEIIAFGRLEERSINTEWVACSVSDQFTHLAWINTPRQGGLGPIRIPPLSDL 180

Qy 181 THQISKDGYVYLEDSGTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFQYTDK 240

Db 181 THQISKDGYVYLEDSGTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFQYTDK 240

Qy 241 HGEVCAGWKPGSETIIPDPAGKLKFDKLN 271

Db 241 HGEVCAGWKPGSETIIPDPAGKLKFDKLN 271

RESULT 6
 ABB57947
 ID ABB57947 standard; Protein; 242 AA.

AC ABB57947;
 XX
 XX
 DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 633.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

XX PN WO200171042-A2.

PD 27-SEP-2001.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PW, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL02050.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions -
 XX
 Disclosure; SEQ ID NO 633; 21pp + sequence listing; English.
 PS
 XX
 The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
 sequences (AB01840-ABL6175) and the encoded proteins
 CC (ABB7737-ABB7707).
 The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 Sequence 242 AA:
 Query Match 59.3%; Score 854.5; DB 22; Length 242;
 Best Local Similarity 65.2%; Pred. No. 4.5e-84; Gaps 2;
 Matches 161; Conservative 29; Mismatches 48; Indels 9;
 QY 25 LLLFLPILPAGAVQGWEETEPRTRERECHFVAGQVYPGEASRSVADHSIHLSSAKISKP 84
 Db 5 LSVLLSAAALVGAARKED----NSCYSHFAGGSYYPDQPK---GDHQIQTAVISKP 55
 QY 85 APYWGSGTAVIDGEKFLKLTDYRGKYLVFFYPLDFTEVCPTEIAFGDLEERSINTE 144
 Db 56 APQFEGTAVVNEKVKLSSLQYLGKVWLFLYPLDFTFVCPTEIAFSDRIAFEKKITE 115
 QY 145 VVACCVSDQSTPFLAWINTPREGGLGPIRPLSDLTHQTSKDXGYVLEDGHTURGLF 204
 Db 116 VIGVSDSHFTHLAWINTPREGGLGDKVPLSLDTHKISKDYGVYLESSGHALRGFLT 175
 QY 205 IDDKGILRQITLNDLPGRSVDETLRLVQAFQYTDKHEVCAGPKPGSETIIPDPAGKL 264
 Db 176 IDQTCVYLRLQITLNDLPGRSVDETLRLVQAFQYTDKHEVCAGPKPGSETIIPDPAGKL 235
 QY 265 KYFDKLN 271
 Db 236 KYFKANN 242
 RESULT 7
 AAB43528
 ID AAB43528 standard; Protein; 233 AA.
 XX
 AC AAB43528;
 XX
 DT 08-FEB-2001 (first entry)
 DE Human cancer associated protein sequence SEQ ID NO:973.
 XX
 Human; cancer associated gene; cancer antigen; detection; cancer;
 KW diagnosis; cyrostatic; proliferative; pulmonary; immunomodulator;
 KW antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
 KW dermatological; neuroprotective; thrombolytic; coagulant; nortropic;
 KW vasoconstrictor; antiangiogenic; gene therapy; inflammation;
 KW immune disorder; haemopoietic cell disorder; autoimmune disorder;
 KW allergic reaction; graft versus host disease; organ refection;
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;
 KW neurological disease; drug screening.
 OS Homo sapiens.
 XX
 PN WO200055350-A1.
 XX
 PD 21-SEP-2000.
 XX
 PR 08-MAR-2000; 2000WO-US05882.
 XX
 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI: 2000-58753/55.
 XX
 DR N-PSDB; AAC77737.
 CC Novel isolated nucleic acids comprising sequences encoding peptides
 PT useful for treating or diagnosing e.g. cancer -
 XX
 PS Claim 11; Page 1542-1543; 235pp; English.
 XX
 AAC77607 to ACT78448 encode the human cancer associated proteins given
 CC in AAB43398 to AAB44239. The proteins can have activities based on the
 CC tissues and cells the genes are expressed in. Example of activities
 CC include: cytostatic; prodrugs; vulnery; immunomodulator;
 CC antiidiabetic; antiasthmatic; antirheumatic; antiarthritic;
 CC antitumour; antithyroid; antiallergic; antibacterial; antiviral;
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
 CC nootropic; vasoconstrictor; antipsoriatic and antiangiogenic. The
 CC polynucleotides and polypeptides can be used for preventing, treating or
 CC ameliorating medical conditions and diagnosing pathological conditions.
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
 CC the present invention may be used to treat immune disorders by activating
 CC or inhibiting the proliferation, differentiation or mobilisation of
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune
 CC disorders, allergic reactions, graft versus host disease and organ
 CC rejection, modulate haemostatic or thrombolytic activity, modulate
 CC inflammation, cancers, cardiovascular disorders, neurological disease and
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to
 CC AAC8457 and AB42420 represent sequences used in the exemplification of
 CC the present invention.
 XX
 Sequence 233 AA:
 Query Match 52.1%; Score 750.5; DB 21; Length 233;
 Best Local Similarity 67.1%; Pred. No. 8e-73; Gaps 1;
 Matches 139; Conservative 27; Mismatches 40; Indels 1; Gaps 1;
 QY 64 ASRVSVADHSIHLSSAKISKPAPYNGEGTAVI-DGFFKELKLTDYRGKYLFFFYPLDFE 122
 Db 25 ATCGVGTADRKMSGGNAKIGHAPNPKTAYMPDGDQPKDLSLSDYKGKVYFFFYPLDFE 84
 QY 123 VCPTEIAFGDLEERSINTEVACVSDSFTLAWINTPREGGLGPIRPLSDLTH 182
 Db 85 VCPTEIAFGDLEERSINTEVACVSDSFTLAWINTPREGGLGPIRPLSDLTH 144
 QY 183 QISKDYGVYLEDGHTURGLFIDDKGILRQITLNDLPGRSVDETLRLVQAFQYTDKHE 242
 Db 145 TIAQDYGVLRADEGTSFRGFLFIDDKGILRQITVNDLPGRSVDETLRLVQAFQYTDKHE 204
 QY 243 EVCPAGWKPGSETIIPDPAGKLKYDK 231
 Db 205 EVCPAGWKPGSETIIPDPAGKLKYDK 231
 RESULT 8
 ABP41353
 ID ABP41353 standard; Protein; 233 AA.
 XX
 AC ABP41353;
 XX
 DT 23-AUG-2002 (first entry)
 DE Human ovarian antigen HCO001, SEQ ID NO:2485.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder; KW gastrointestinal disorder; urinary system disorder; drug screening; KW gene therapy; chromosome mapping; forensic analysis; KW antibody preparation; cyostatic; immunomodulatory; neuroprotective; KW antiinflammatory; gynaecological; reproductive; chromosome 1p34.1; XX OS Homo sapiens.

XX WO200200677-A1.

XX PD 03-JAN-2002.

XX PF 07-JUN-2001; 20001W0-US18569.

XX PR 07-JUN-2000; 2000US-209467P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Birse CE, Rosen CA;

XX DR WPI; 2002-147878/79.

XX DR N-PSDB; AB054430.

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

XX PS Claim 11; SEQ ID No 2485; 2922pp; English.

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also encompasses polypeptides 90% identical and poly nucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vector and host cells comprising human ovarian antigens, poly nucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen poly nucleotides and polypeptides in diagnosing, treating, prognosis or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility), disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea, endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic shock syndrome, inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and poly nucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The poly nucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 233 AA;

Query Match 52.1%; Score 750.5; DB 23; Length 233; Best Local Similarity 67.1%; Pred. No. 8e-73; Mismatches 139; Matches 139; Conservative 27; Mismatches 40; Indels 1; Gaps 1;

QY 64 ASRVADHSLSLAKSKAKSKPAPYWEGSTAVI-DGERERKELKDYRGKLVLFVFFYPLDFTF 122

Db 25 ATCVGTAQDRKMSMSGNAIGHPAPNFKATAVMPDQGQFDISLSDYKGKVWFFYPLDFTF 84

QY 123 VCPTEITAFGDRIEFSINTEVACVSDQFTHLAWINTRRQGGGPIRPLSDLTH 182

Db 85 VCPTEITAFSDRAEFLKLNQVIGASVDSHFLAWINTPKQGGGPMNIPLSDPKR 144

XX Sequence 198 AA;

Query Match 51.8%; Score 746; DB 22; Length 198; Best Local Similarity 70.5%; Pred. No. 2e-72; Mismatches 136; Matches 136; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

QY 79 AKTSKAPYWEGSTAVIIGEFEKELKDYRGKLVLFVFFYPLDFTFVCTEITAFGDRIEFL 138

Db 6 ARIGKAPADPDFKATAVVGFKEVLSKDSYKGKVWFFYPLDFTFVCPTEITAFSDRAEFD 65

QY 139 RSINTEVACVSDQFTHLAWINTPRQGGGPIRPLSDLTHQTSKDYGVSLEDSGHT 198

Db 66 RKLGEVLFVGSVSDQFTHLAWINTPRQGGGPLNPLAIVTRRUSIDCIGVLLKDEGIA 125

Qy	199 LRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOQYTDKHGIVCAGWKPGSETIIP 258
Db	126 YRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOQYTDKHGIVCAGWKPGSETIIP 185
Qy	259 DPAGKLKYFDKL 271
Db	186 NVDDSKEYFSKH 198
RESULT 10	
AAB6040	
ID AAB6040 standard; peptide; 198 AA.	
XX	
AC AAB6040;	
XX	
DT 29-JUN-2001 (first entry)	
XX	
DE Amino acid sequence of the acid form of peroxiredoxin TDx2.	
XX	
DE Peroxiredoxin; acid form; oxidative stress; cell death; cancer;	
XX	
KW autoimmune disease; neurodegeneration; metabolic disorder.	
XX	
OS Homo sapiens.	
XX	
PN FR2798672-A1.	
XX	
PD 23-MAR-2001.	
XX	
PF 17-SEP-1999; 99FR-0011663.	
XX	
PR 17-SEP-1999; 99FR-0011663.	
XX	
(COMS) COMMISSARIAT ENERGIE ATOMIQUE.	
XX	
PI Rabilloud T;	
XX	
DR WPI; 2001-259869/27.	
XX	
PT Purified acid form of peroxiredoxin, a marker of oxidative stress, useful in diagnosis and for identifying potential apoptotic and anti-apoptotic agents comprises a specific amino acid motif close to the active site	
XX	
PS Claim 12; Page 25-26; 28pp; French.	
XX	
CC The present sequence represents the acid form of a human peroxiredoxin enzyme. The acid form of peroxiredoxin is a characteristic marker of oxidative stress that can be measured simply and quickly, providing a reliable indication of stress even where this is of short duration. Modulators of the acid form of peroxiredoxin enzyme are used for the stimulation or inhibition of apoptosis. Compounds that stimulate formation of the acid form of peroxiredoxins are used to induce cell death (treatment of cancer and autoimmune diseases) while those that inhibit its formation are used to prevent cell death (treatment of neurodegeneration). Measuring the ratio between acid form and the native form of peroxiredoxin is used to diagnose metabolic disorders associated with oxidative stress.	
XX	
SQ Sequence 198 AA;	
Query Match 50.0%; Score 721; DB 22; Length 198;	
Best Local Similarity 69.8%; Pred. No. 1; Le-69; 31; Indels 2; Gaps 2; Matches 134; Conservative 25; Mismatches 31; Indels 2; Gaps 2;	
Db 6 AHIGKSAFPDTAVWDYQAFKIKLSDRGKVWLFYPLDFTFCPTETIAFSDAEE 65	
Qy 79 AKISKPAPWEGTAVIDGEGFRELKLDYRGKLVFFYPLDFTFCPTETIAFGDRLEE 137	
Db 6 AKIGHPAPNFKKATAVMDQGFFRDISLSDYKGVWVFFYPLDFTFCPTETIAFSDAEE 65	
Qy 139 RSINTEVVACSVDSQFTHLAWNTPRRQGPGGKPIRPLSLDTHQISKDYGVYLEDSGHT 198	
Db 66 RKGCLFVLLGVSVDSQFTHLAWNTPRKGGGLAPLNPLAIVTKSLSQNYGVLNDEGA 125	
Qy 138 PRSINTEVVACSVDSQFTHLAWNTPRRQGPGGKPIRPLSLDTHQISKDYGVYLEDSGHT 197	
Db 66 EFKLNGCQVIGASVDSHFLAWNTPKQGGLGPMNIPLVSDPKRTIAQDYGVVKADEGI 125	
Qy 198 TURGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOQYTDKHGIVCAGWKPGSETIIP 257	
Qy 259 DPAGKLKYFDKL 271	
RESULT 11	
AAU78580	
ID AAU78580 standard; Protein; 198 AA.	
XX	
AC AAU78580;	
XX	
DT 05-JUN-2002 (first entry)	
XX	
DE Mouse peroxiredoxin II-1 (PrxII-1) protein.	
XX	
KW Peroxiredoxin; Prx; promoter; PrxII-1.	
XX	
MU SP.	
XX	
FR Key Location/Qualifiers	
FT Misc-difference 7 /note= "Encoded by CAA"	
FT Misc-difference 97 /note= "Encoded by GGC"	
XX	
PN KR99066020-A.	
XX	
PD 16-AUG-1999.	
XX	
PF 20-JAN-1998; 98KR-0001604.	
XX	
PR 20-JAN-1998; 98KR-0001604.	
XX	
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.	
XX	
PI Yeom YI, Lim MJ, Lee GG, Yoo DY;	
XX	
DR WPI; 2000-547264/50.	
PT N-PSDB; AB47315.	
XX	
PT Peroxiredoxin PRX II-1 and promoter derived from mouse, base sequence of PRX II-2 and PRX II-3 -	
XX	
PS Disclosure; Fig 6; 14pp; English.	
XX	
CC This invention relates to the sequence of the mouse peroxiredoxin II-1 (PrxII-1) promoter. The invention also comprises the cDNA sequences encoding the mouse PrxII-1, PrxII-2 and PrxII-3 proteins. The present sequence represents the mouse peroxiredoxin protein sequence of the invention.	
CC	
SQ Sequence 198 AA;	
Query Match 49.9%; Score 719; DB 21; Length 198;	
Best Local Similarity 68.9%; Pred. No. 1; Le-69; 31; Indels 0; Gaps 0; Matches 133; Conservative 22; Mismatches 38; Indels 0; Gaps 0;	
Qy 79 AKISKPAPWEGTAVIDGEGFRELKLDYRGKLVFFYPLDFTFCPTETIAFGDRLEE 138	
Db 6 AHIGKSAFPDTAVWDYQAFKIKLSDRGKVWLFYPLDFTFCPTETIAFSDAEE 65	
Qy 139 RSINTEVVACSVDSQFTHLAWNTPRRQGPGGKPIRPLSLDTHQISKDYGVYLEDSGHT 198	
Db 66 RKGCLFVLLGVSVDSQFTHLAWNTPRKGGGLAPLNPLAIVTKSLSQNYGVLNDEGA 125	
Qy 199 LRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOQYTDKHGIVCAGWKPGSETIIP 258	
Db 126 YRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOQYTDKHGIVCAGWKPGSETIIP 185	

Db	186	:	NUVDSKEIFSKHN	198	Db	183	PTKSKEYFE	191	
RESULT 12									
ABBS58322	ID	ABBS58322	standard: Protein;	194 AA.	XX	XX	RESULT 13		
XX	XX	XX			XX	XX	ABBS58323		
AC	AC	AC			XX	XX	ID	ABBS58323	
XX	XX	XX			XX	XX	standard: Protein;	194 AA.	
DE	DE	DE	Drosophila melanogaster	polypeptide SEQ ID NO 1758.	XX	XX	DE	Drosophila melanogaster	
KW	KW	KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.		XX	XX	KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.	
OS	OS	OS	Drosophila melanogaster.		OS	OS	OS	Drosophila melanogaster.	
XX	XX	XX	W0200171042-A2.		XX	XX	XX	W0200171042-A2.	
XX	XX	XX	PD	27-SEP-2001.	XX	XX	XX	PD	
XX	XX	XX	PF	23-MAR-2001; 2001WO-US09231.	XX	XX	PF	23-MAR-2001; 2001WO-US09231.	
XX	XX	XX	PR	23-MAR-2000; 2000US-191637P.	XX	XX	PR	23-MAR-2000; 2000US-191637P.	
XX	XX	XX	PR	11-JUL-2000; 2000US-0614150.	XX	XX	PR	11-JUL-2000; 2000US-0614150.	
PA	PA	PA	(PEKE) PE CORP NY.		PA	PA	PA	(PEKE) PE CORP NY.	
XX	XX	XX	PI	Venter JC, Adams M, Li PWD, Myers EW;	XX	XX	PI	Venter JC, Adams M, Li PWD, Myers EW;	
XX	XX	XX	DR	WPI; 2001-656860/75.	XX	XX	DR	WPI; 2001-656860/75.	
DR	DR	DR	N-PSDB; AB02425.		DR	DR	DR	N-PSDB; AB02425.	
XX	XX	XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -	XX	XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -	
PS	PS	PS	Disclosure; SEQ ID NO 1758; 21pp + Sequence Listing; English.		PS	PS	PS	Disclosure; SEQ ID NO 1761; 21pp + Sequence Listing; English.	
CC	CC	CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB0116176-AB0130511), expressed DNA sequences (AB011840-AB0116175) and the encoded proteins (AB057737-AB072072).		CC	CC	CC	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB0116176-AB0130511), expressed DNA sequences (AB011840-AB0116175) and the encoded proteins (AB057737-AB072072).	
CC	CC	CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.		CC	CC	CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	
CC	CC	CC	XX	Sequence 194 AA;	XX	XX	XX	Sequence 194 AA;	
SQ	SQ	SQ	Query Match 49.6%; Score 715; DB 22; Length 194; Best Local Similarity 68.3%; Pred. No. 4.4e-69; Matches 129; Conservative 29; Mismatches 31; Indels 0; Gaps 0;		Query Match 49.6%; Score 715; DB 22; Length 194; Best Local Similarity 68.3%; Pred. No. 4.4e-69; Matches 129; Conservative 29; Mismatches 31; Indels 0; Gaps 0;		Query Match 49.6%; Score 715; DB 22; Length 194; Best Local Similarity 68.3%; Pred. No. 4.4e-69; Matches 129; Conservative 29; Mismatches 31; Indels 0; Gaps 0;		
Qy	Qy	Qy	80 KISKAPWEGAVIDEEFKELKLTDYRGKLYVFFYPLDFPFVCPHEIIFGDRLEFR 139		Qy	80 KISKAPWEGAVIDEEFKELKLTDYRGKLYVFFYPLDFPFVCPHEIIFGDRLEFR 139		Qy	80 KISKAPWEGAVIDEEFKELKLTDYRGKLYVFFYPLDFPFVCPHEIIFGDRLEFR 139
Db	Db	Db	3 QLOKPAFAPAGTAWNGVFKDKLSDYKRGKLYVFLVLFPLDFPFVCPHEIIFGDRLEFR 62		Db	3 QLOKPAFAPAGTAWNGVFKDKLSDYKRGKLYVFLVLFPLDFPFVCPHEIIFGDRLEFR 62		Db	3 QLOKPAFAPAGTAWNGVFKDKLSDYKRGKLYVFLVLFPLDFPFVCPHEIIFGDRLEFR 62
Qy	Qy	Qy	140 SNTTEVWACSVSQTFLAWINTPRRGGLGPIRIPULSDLTHQISKDGYLGYLEDSGHTL 199		Qy	140 SNTTEVWACSVSQTFLAWINTPRRGGLGPIRIPULSDLTHQISKDGYLGYLEDSGHTL 199		Qy	140 SNTTEVWACSVSQTFLAWINTPRRGGLGPIRIPULSDLTHQISKDGYLGYLEDSGHTL 199
Db	Db	Db	63 KINCEVIGCSTDSDQFLTHLAWINTPRKGGLGSMIDPLADSKMVKARDYGVLDENGIPF 122		Db	63 KINCEVIGCSTDSDQFLTHLAWINTPRKGGLGSMIDPLADSKMVKARDYGVLDENGIPF 122		Db	63 KINCEVIGCSTDSDQFLTHLAWINTPRKGGLGSMIDPLADSKMVKARDYGVLDENGIPF 122
Qy	Qy	Qy	200 RGLFLIDDKGLRQITLNDLPGRSVDETLRQVQAFYTDKGEVCPAGWPGSEIIPD 259		Qy	200 RGLFLIDDKGLRQITLNDLPGRSVDETLRQVQAFYTDKGEVCPAGWPGSEIIPD 259		Qy	200 RGLFLIDDKGLRQITLNDLPGRSVDETLRQVQAFYTDKGEVCPAGWPGSEIIPD 259
Db	Db	Db	123 RGLFLIDDKQNLRQITVNDLPGVRSVEETLRQVQAFYTDKGEVCPANWPGQKTMVAD 182		Db	123 RGLFLIDDKQNLRQITVNDLPGVRSVEETLRQVQAFYTDKGEVCPANWPGQKTMVAD 182		Db	123 RGLFLIDDKQNLRQITVNDLPGVRSVEETLRQVQAFYTDKGEVCPANWPGQKTMVAD 182
Qy	Qy	Qy	260 PAGKLKYFD 268		Qy	260 PAGKLKYFD 268		Qy	260 PAGKLKYFD 268
..	: :	
Db	183	PTKSKEYFE	191		Db	183	PTKSKEYFE	191	

RESULT 14
 AAW093
 ID AAW09793 standard; Protein: 199 AA.
 XX
 AC
 XX
 DT 10-JUN-1997 (first entry)
 XX
 DE Natural killer cell enhancing factor A.
 DE
 DE Homo sapiens.
 KW NKEF-A; NKEF-B; natural killer cell enhancing factor; protect;
 KW mixed metal-thiol oxidative inactivation; increase activity;
 KW enhancement; stimulate; interleukin-2; IL-2; lymphocyte activation;
 KW proliferation; combined immunotherapy; cytokine.
 XX
 OS Homo sapiens.
 XX
 PN US5610286-A.
 XX
 PD 11-MAR-1997.
 XX
 PF 04-NOV-1991; 91US-0787148.
 XX
 PR 31-AUG-1994; 94US-0299162.
 PR 04-NOV-1991; 94US-0787148.
 PR 03-MAY-1994; 94US-0232189.
 XX
 PA (REGC) UNTV CALIFORNIA.
 XX
 PT Golub SH, Shau H;
 XX
 DR WPI; 1997-178453/16.
 DR N-PSDB; AAF62696.
 XX
 PT DNA encoding natural killer cell enhancing factors - protects
 PT enzymes from metal-thiol oxidative inactivation and increases the
 PT activity of natural killer cells
 XX
 PS Claim 1; Column 21-24; 18PP; English.
 CC AAW09793-94 are the amino acid sequences for natural killer cell
 CC enhancing factors (NKEF) A and B respectively. The DNA (AAF62696-97)
 CC encoding them is useful for prodn. of recombinant NKEF A and B, which may
 CC have the same biological activities as native NKEF. Native NKEF protects the
 CC enzymes from mixed metal-thiol oxidative inactivation and increases the
 CC activity of NK cells when used alone or in combinations with other NK
 CC cell enhancement proteins, e.g. interleukin (IL) 2. It is useful in
 CC in-vivo and in-vitro applications where it is desirable to stimulate NK
 CC cell activity and is effective with IL-2 in inducing lymphocyte
 CC activation and proliferation and thus may be used for combined
 CC immunotherapy with cytokines, e.g. IL-2, TNF or interferon, to increase
 CC the function of B cells, T cells, macrophages, NK cells and other
 CC leukocytes.
 XX
 SQ sequence 199 AA;
 Query Match 49.5%; Score 713.5; DB 18; Length 199;
 Best Local Similarity 68.8%; Pred. No. 6.e-9;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;
 Sequence 224 AA;
 Qy 79 AKISKPAPWGGSTAVI-DGEFKELKLTDYRKLYVFFYPLDFTVCPTETIAFGDLRE 137
 ||||| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 6 AKIGHAPAPNPKATAVMPDGQFRKDISLSDYKGKGVVFFFPFLPFTFCVCPTEIAFSDRAEE 65
 Qy 138 FRSINTEVVACSVSDQFTHLAWINTPRROGGIPRIPRLSDLTHQISKDGYVYLEDGH 197
 || : || : ||| : |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 66 PFKLNGQVIGASVDFSHCFLAWNTKKQKGSPNPLIPNSDKPRAIQDGYVYLEDGH 125
 Qy 198 TURGLFIDDKGILRQTLNDPLPGVRSVDETRLVLQAQYQDTHKGHEVCPACKWPSSETII 257
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 126 SFRGLFIIDDKGILRQITVNDPCCRSVDETRLVLVOAFOFIDKHKHGEVCPAGWKGPSDTIK 185
 Qy 258 PDPAGKLKVYFDK 269
 ||| : |||:
 Db 186 PDVPKTKYEFSK 197
 RESULT 15
 AAB5659
 ID AAB5659 standard; Protein: 224 AA.
 XX
 AC AAB5659;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1537.
 XX
 KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardiotropic; immunomodulatory; muscular;
 KW vulnery; antibacterial; gene therapy; nephrotropic; antiinfective; gynaecological;
 KW gastrointestinal; pulmonary; neural; immune; reproductive; renal;
 KW wound; infectious disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2000055174-A1.
 XX
 PR 12-MAR-1999; 99US-0124220.
 PR 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-0505988.
 XX
 PT Rosen CA, Ruben SM;
 XX
 DR WPI; 2000-587513/55.
 DR N-PSDB; AAF16162.
 XX
 PT Prostate cancer associated gene sequences, referred to as prostate
 PT cancer antigens, useful for treatment, prevention, and diagnosis of
 PT disorders such as prostate cancer.
 XX
 PS Claim 11; Page 1979; 2338pp; English.
 CC AAF1556 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB6363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardiotropic, immunomodulatory, muscular, vulnery, gastrointestinal,
 CC nephrotropic, antiinfective, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen
 CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention.
 XX
 Sequence 224 AA;
 Query Match 48.8%; Score 703; DB 21; Length 224;
 Best Local Similarity 66.5%; Pred. No. 1.e-67;
 Matches 127; Conservative 28; Mismatches 36; Indels 0; Gaps 0;
 Qy 81 ISKPAPWGGAVIDGEEFKELKLTDYRKLYVFFYPLDFTVCPTETIAFGDLREFS 140
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
 Db 33 VTHQAPYFKGTVANGEFKFLSDLDDFKGKLYVLFYPLDFTFCVCPTEIAFSDKANEFH 92
 Qy 141 INTEVVACSVSDQFTHLAWINTPRROGGIPRIPRLSDLTHQISKDGYVYLEDGSHLR 200

Db 93 :| |||| |||| |:||||||| :| ||| :| ||||| |||:||| ||| ||| |||
VNC EVA VAS VDS HESHL AWN TPRK NGG HMTA LSL DTK QIS RDY GV L EGG SGL AR 152
QY 201 GLF IID DKG ITR QIT LND LPV GR S D E T L R L V Q A F Q Y T D K H G E V C P A G W K P G S E T I P D P 260
Db 153 GLF IID P N G V I K H L S N D L P V G R S V E T L R L V K A Q Y V E T H G E V C P A N W I P D S P T I K P S P 212
QY 261 AGK L K Y F D K L N 271
Db 213 RAS K E Y F O K V N 223

Search completed: January 17, 2003, 19:18:23
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:16:47 ; search time 35 seconds

Scoring table: BIOSIM62 Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 266047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBL_21:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp Rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

1 1296 89.9 274 6 Q9BG12 Q9bg12 bos taurus

2 1265.5 87.9 273 11 Q9z0v5 Q9z0v5 rattus norv

3 877.0 60.9 223 Q9Bf6 Q9bf6 biomphalaria

4 854.5 59.3 242 5 Q9i3q4 Q9i3q4 drosophila

5 749.5 52.0 199 6 Q9Bt3 Q9bt3 bos taurus

6 734.0 50.9 199 5 Q9r082 Q9r082 globodera r

7 733.0 50.9 198 11 Q9Cwj4 Q9cj4 mus musculu

8 727.5 50.5 198 11 Q98376 Q98376 mus musculu

9 723.5 50.2 199 11 Q9kyl Q9kyl cricetus

10 721.5 50.1 199 6 Q9Bt4 Q9bt4 bos taurus

11 721.5 50.0 199 13 Q93241 Q93241 cyprinus ca

12 721.0 50.0 195 5 Q9n198 Q9n198 ascaris suu

13 718.5 49.9 199 11 Q90W12 Q9cw12 mus musculu

14 718.0 49.8 198 11 Q9B49 Q9db49 mus musculu

15 717.0 49.8 196 5 Q9usf6 Q9usf6 aedes aegy

16 715.0 49.6 194 5 Q9i3p0 Q9i3p0 drosophila

Summaries

RESULT 1

Q9G12 ID Q9G12 PRELIMINARY; PRT; 274 AA.

AC Q9G12; DT 01-JUN-2001 (TREMBL; 17, Created)

DT 01-JUN-2001 (TREMBL; 17, Last sequence update)

DT 01-DEC-2001 (TREMBL; 19, Last annotation update)

DE Peroxiredoxin 4.

OS Bos taurus (Bovine).

RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

RT Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

RL Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Levens G., Donnay I., Knoops B.;

RT Cloning of 4 new bovine peroxiredoxins, and screening of the complete

RL peroxiredoxin (SPR-2000) family in different bovine tissues.";

DR Submitted (SPR-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AR305563; ARG533600.1; -.

DR HSSP; P30041; IPRX.

DR InterPro;

DR Pfam; PF00578; APc-TSA; 1.

SQ SEQUENCE 274 AA; 30741 MW; AEI4176CF1C70E37 CRC64;

Query Match 89.9%; Score 1296; DB 6; Length 274; Best Local Similarity 92.1%; Pred. No. 2.7e-116; Matches 246; Conservative 8; Mismatches 13; Indels 0; Gaps 0; Gaps 0;

QY 5 PLLAATTDPDHGRHRRRLPLPLFLFLPAGAVOCWETEPRPRTEECFYAGCQVYGEA 64

Db 8 PPLAATTDPDHGRHRRRLPLPLFLFLPAGAVOCWETEPRPRTEECFYAGCQVYGEA 67

QY 65 SRVSYADHSILHSKAKISKPKAPYWEGTAVIDGFFKEKLTDYRGKYUVFFYPLDFFVC 124

Db 68 SRVSYAEHSILHSKAKISKPKAPYWEGTAVINGEKFKLTDYRGKYUVFFYPLDFFVC 127

QY 125 PTEIIFGDRLEFRSINTEVWACSVSDQFTHIAWINTPRROGGPTRIPLSLDTHQI 184

Q8wq02 ostertagia

Q92655 oncorehynchus

Q91886 oncorehynchus

Q91265 caenorhabdit

Q76452 onchocerca

Q81416 acanthochei

Q84941 onchocerca

Q16026 dirofilaria

Q94365 onchocerca

Q94621 litocephala

Q96ub2 litocephala

Q16006 dirofilaria

Q920v6 rattus norv

Q9gnf6 schistosoma

Q816c4 echinococcus

Q9jej0 dirofilaria

Q9gpq3 dirofilaria

Q96380 echinococcus

Q9u47 trypansom

Q9469 trypansom

Q74887 schizosach

Q97161 schistosoma

Q99u89 leishmania

Q9u1b5 leishmania

Q9fe86 chlamydomon

Q96763 trypansom

Q9fns2 chlamydomon

Q8vsh1 trypansom

Q910d3 schistosoma

Q9tzs4 leishmania

Q8ync5 anabena sp

Db	128	PTEITAFGDRIDERSINTEVACSVSDSQTFLHANINTPRRQGLGSINIPFLADLNHQI	187	OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Qy	185	SKDYGVYLEDSGHTLRLGLFTIDDKGILTRQITLNDLIPVGRSVDETLRLVQAFQYTDKHGEV	244	OC	Planorbidae; Biomphalaria.
Db	188	SKDYGVYLEDSGHTLRLGLFTIDDKGILTRQITLNDLIPVGRSVDETLRLVQAFQYTDKHGEV	247	OX	NCBI_TaxID:6526;
Qy	245	CPAGWKPGSEPIIPDPAGKLYFDFKLN	271	RN	[1]
Db	248	CPAGWKPGSEPIIPDPAGKLYFDFKLN	274	RP	SEQUENCE FROM N. A.
RESULT 2					
O9Z0V5		PRELIMINARY;		RA	STRAIN=LAC; TISSUE=ALBUMEN GLAND;
ID	O9Z0V5	PRT;	273 AA.	RA	Cousin C., Ofori K., Okulate M., Grant J., Richards C., Lewis F.,
AC	O9Z0V5;			RT	Knight M.;
DT	01-MAY-1999	(TREMBREL. 10, Created)		RT	"Biomphalaria glabrata: Molecular differences between the albumen
DT	01-MAY-1999	(TREMBREL. 10, Last sequence update)		RT	glands of susceptible and non-susceptible snails";
DT	01-JUN-2001	(TREMBREL. 17, Last annotation update)		RL	Submitted (JAN 2001) to the EMBL/GenBank/DBU databases.
DE	PRX IV.			DR	EMBL; AY02625; AAK6236_1; -.
GN	PRX IV.			DR	HSSP; P30041; PRX.
OS	Rattus norvegicus (Rat).			DR	IntePro; IPR00866; Ahpc-TSA.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			KW	Pfam; PRO0578; Ahpc-TSA; 1.
OX	NCBI_TaxID=10116;			FT	Peroxidase.
RN	[1]			SQ	SEQUENCE 223 AA; 1 1 25035 MW; B5B995442C1BF906 CRC64;
RP	SEQUENCE FROM N. A.			GN	Query Match 60.9%; Score 877; DB 5; Length 223;
RX	MEDLINE:99144808; PubMed=10025941;			QY	Best Local Similarity 76.5%; Pred. No. 3.7e-76;
RA	Matsumoto A., Okado A., Fujii T., Fujii J., Egashira M., Nikawa N.,			DB	Matches 163; Conservative 18; Mismatches 30; Indels 2; Gaps 1;
RA	Taniguchi N.; Cloning of the peroxiredoxin gene family in rats and characterization			QY	55 AGQQVYPGRRSRSVADHSIHLASKAKISHPAPWEGTAVIDGERFELKLTDYRGKYLFF 114
RT	of the fourth member. " FEBS Lett. 443: 246-250 (1999).			DB	5 AGGGVPOEIKR-T-TIGHUQWQSIVASRKPAPDNGTAVIKGERFDKISDFKGKYLFF 62
RL	DR			QY	115 FYPADFTVCPTEIAFGDRDEERSINTEVACSVSDQFTHLAWINTPRRQGIGPRL 174
DR	EMBL; AP106945; RADD1793.1; -.			DB	63 FYPLDFTVCPTEIAFGDRDEERSINTEVACSVSDQFTHLAWINTPRRQGIGKINY 122
DR	HSSP; P30041; PRX.			QY	175 PLISDLTHQSKDYGVYLEDSGHTLRLGLFTIDDKGILTRQITLNDLIPVGRSVDETLRLVQ 234
DR	InterPro; IPR00866; Ahpc-TSA.			DB	123 PLISDITHESKAYGVYLQDGLHSRLGLFTIDPKGLTRQITMNDLIPVGRSVDETLRLVQ 182
DR	Pfam; PF00578; Ahpc-TSA; 1.			QY	235 FQYTDKHGECVCPAGWKPGSEPIIPDPKSKYF 267
SQ	SEQUENCE 273 AA; 31007 MW; 09E614794F1DC6C2 CRC64;			DB	183 FQYTDKHGECVCPAGWKPGSEPIIPDPKSKYF 215
Query Match 87.9%; Score 1266.5; DB 11; Length 273;					
Best Local Similarity 90.3%; Pred. No. 1.8e-113; Mismatches 13; Indels 3; Gaps 2;					
Matches 242; Conservative 10; Mismatches 13; Indels 3; Gaps 2;					
RESULT 3					
O9Y3Q4		PRELIMINARY;	PRT;	242 AA.	
ID	O9Y3Q4				
AC					
DT	01-MAY-2000	(TREMBREL. 13, Created)			
DT	01-MAY-2000	(TREMBREL. 13, Last sequence update)			
DT	01-JUN-2001	(TREMBREL. 19, Last annotation update)			
DE	CG1274 protein (SECRETABLE thioredoxin peroxidase) (GH25379P).				
GN	JARRAC2 OR CG1274.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;				
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
OC	Ephydriidea; Drosophilidae; Drosophila.				
OX	NCBI_TaxID=7227;				
RN	[1]				
RP	SEQUENCE FROM N. A.				
RC	STRAIN=BERKELEY;				
RX	MEDLINE=20196005; PubMed=10731132;				
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,				
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,				
RA	George R.A., Lewellen S.E., Richards S., Ashburner M., Henderson S.N.,				
RA	Sutton G.G., Wostman J.R., Yandell M.D., Zhang Q., Chen L.X.,				
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,				
RA	Abrial J.F., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,				
RA	Baldwin D., Balow J.H., Dooley C., Baxendale J., Bayraktaroglu L., Beasley E.M.,				
RA	Beezon K.V., Benos P.V., Brannard B.P., Bolshakov S.,				
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotman P.,				
RA	Burtis K.C., Busam D.A., Butler J., Cadieu E., Center A., Chandra I.,				
RA	Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,				
RA	de Pablo J., Delcher A., Deng Z., May S., Diefenbach J., Dietz S.M.,				
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,				
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,				

RA Posler C., Gabrieleian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Hayve D., Heiman T.J., Hernandez J.J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeewam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.C., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod J., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Mozny D.M., Nelson D.R.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussekern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos T., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svistkova R., Tector R., Turner R., Venner E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodward T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL *Science* 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20098324; PubMed-10632718;
 RA Rodriguez J., Agudo M., van Damme J., Vandekerckhove J.,
 RA Santaren J.F.,
 RT "Polypeptides differentially expressed in imaginal discs define the
 family of genes in *drosophila*,"
 RL *Eur. J. Biochem.* 267:487-497(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Raduuk S.N., Spinola B., Klichko V.I., Orr W.C.,
 RT "Cloning, expression and characterization of the peroxiredoxin gene
 submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Aspaziani A., Carlson J.,
 RA Champé M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA González M., Guarín H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuño J., Paciell J., Paragas V., Park S., Phoumanenavong S., Wan K.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AE033476; RAF47704.1; -;
 DR EMBL: AF42986.1; -;
 DR EMBL: AF221614; AX00679.1; -;
 DR EMBL: AX00785; AAL28333.1; -;
 DR Flybase; FBgn0040308; Jefrac2.
 DR InterPro; IPR000866; Abpc-TSA.
 DR Pfam; PF00578; Abpc-TSA.
 KW Peroxidase.
 SQ SEQUENCE 242 AA; 26743 MW; 8A0142FB191D9564 CRC64;
 Query Match 59.3%; Score 854.5; DB 5; Length 242;
 Best Local Similarity 65.2%; Pred. No. 6.1e-74;
 Matches 161; Conservative 29; Mismatches 48; Indels 9; Gaps 2;
 Qy 25 LILFLPLPAGAVQWGMETEERPRTRBEECHYAGQGYPPGEASRVSVADHSIHLRSKAKISP
 ID 6 KAHVSKPAPRERQATAVNDGAFKEVKLSDYKGKVYVLFYPLDFTFVCPREIVAFSDRAAE
 AC 138 FRSLINTEVACSVQDQFTIAWINTPRRQGLGPTRIPPLSLDLHQISKDQYVILEDSGH
 AC 6 FHKLNCEVAGVSQDQFTIAWINTPRRQGLGPTRIPPLSLDLHQISKDQYVILEDSGH 197
 Qy 198 TLRGLFTIDDKGILRQITLNDLPVGRSVDIETLRLVQAFQYTDKIGEVCPAGWKQGETII
 DB 126 AYRGLEVFDGKGVLRQVITNDLPVGRSVDIETLRLVQAFQYTDKIGEVCPAGWKQGETII 257
 Qy 258 PDPACKLVYFDKLN 271
 DB 186 PNVDDSKKEYFSKHN 199
 SQ RESULT 6
 ID 09Y082
 AC 09Y082
 PRELIMINARY; PRT; 199 AA.
 DT 01-NOV-1999 (T-EMBLrel. 12, last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, last annotation update)
 DE Peroxiredoxin.
 GN TPX-1.
 OS Globodera rostochiensis (Golden nematode).
 OC Eukaryota; Metazoa; Nemata; Chromadorea; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
 OC NCBI_TaxID:31243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ROL;
 RC MEDLINE-20542028; PubMed-11087915;
 RA Robertson L., Robertson W.M., Sobeza M., Helder J., Tetaud E.,

205 IDKGILRQITLNDLPVGRSVDIETLRLVQAFQYTDKIGEVCPAGWKQGETIIIDPAGKL 264

RA	Ariyanayagan M.R., Ferguson M.A.J., Fairlamb A., Jones J.T.;
RT	"Cloning, expression and functional characterisation of a peroxiredoxin from the potato cyst nematode <i>Globodera rostochiensis</i> ."
RL	Mol. Biochem. Parasitol. 111:41-49 (2000).
DR	EMBL: AJ243736; CAB48391.1; -
DR	HSSP: P30041; PRX1.
DR	InterPro: IPR00086; AhpC-TSA.
DR	PIam; PF00578; AhpC-TSA; 1.
SO	SEQUENCE 199 AA; 22317 MW; 90AD8274672B0F53 CRC64;
Query Match	50.9%; Score 734; DB 5; Length 199;
Best Local Similarity	67.4%; Pred. No. 1. 8e-62;
Matches	130; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
Query	77 SKAKISKPAPWEGAVIDGEFKEKLTDYRGKVIVFFYPLDFPVFCPEIAGDRLE 136
Db	5 SKAFIGKPKPKFSADAVVNGDFKTSISDDYRGKAVVLFYPLDFPVFCPEIAGDRLE 64
QY	137 EFRSINTEVVACSVDSQFTHAWINWPRROGGGLDRIPLSLDTHQISKDGYVLEDSG 196
Db	65 EFKIDTQTLACSTDSKFSHLEWINKPRKGGLGEMKIPVILADPHNKHISRDYGHMEAG 124
QY	197 HTLRLGLFIIDDKGILRQITNDLPGVRSYDTELRLVQAFQYTDKGEVCPAGWPGSETI 256
Db	125 LAFGLFIDDKGILRQITNDLPGVRSYDTELRLVQAFQYTDKGEVCPAGWPGSETI 184
QY	257 IPDPAGKLKFDFK 269
Db	185 KPDPEGSQTFFGK 197
RESULT 7	
ID	99CW4 PRELIMINARY; PRT; 198 AA.
AC	99CW4; 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	Peroxiredoxin 2.
GN	PRDX2.
OS	Mus musculus (Mouse).
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TAXID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
RX	MEDLINE=11083660; PubMed=11217851;
RA	Kawai J., Shinagawa A., Shiba T., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Miyosawa H., Kondo S., Yamanaoka T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann R., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Mikaido I., Pescce G., Quackenbush J., Scrimml L.M., Stahlb I., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombart P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
RA	"Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690 (2001).
DR	EMBL: AK010653; BAB27093.1; -
DR	HSSP: P30041; PRX2.
DR	MCD: MGI:109486; Prdx2.
DR	InterPro: IPR00086; AhpC-TSA.
DR	PIam; PF00578; AhpC-TSA; 1.
SO	SEQUENCE 198 AA; 21811 MW; 819f9DD77A70259 CRC64;
Query Match	50.5%; Score 727; DB 11; Length 198;
Best Local Similarity	69.4%; Pred. No. 8. 3e-62;
Matches	134; Conservative 23; Mismatches 36; Indels 0; Gaps 0;
Query	79 AKISKPAPWEGAVIDGEFKEKLTDYRGKVIVFFYPLDFPVFCPEIAGDRLE 138
Db	6 AQIGKSAPDTAVVDFGAFKEKLTDYRGKVIVFFYPLDFPVFCPEIAGDRLE 65
QY	139 RSTINTEVACSVDSQFTHAWINWPRROGGGLDRIPLSLDTHQISKDGYVLEDSGHT 198
Db	66 RKGCEVILGVSYDSQFTHAWINWPRROGGGLDRIPLSLDTHQISKDGYVLEDSGHT 125
QY	199 LRLGLFIIDDKGILRQITNDLPGVRSYDTELRLVQAFQYTDKGEVCPAGWPGSETI 258
Db	126 YRLGLFIIDAKGVILRQITNDLPGVRSYDTELRLVQAFQYTDKGEVCPAGWPGSETI 185
QY	259 DPAGKLKFDFK 271
Db	186 NVDDSKEYFSKH 198
RESULT 8	
ID	088376 PRELIMINARY; PRT; 198 AA.
AC	088376; 01-Nov-1998 (Tremblrel. 08, Created)
DT	01-Nov-1998 (Tremblrel. 08, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	Type II peroxiredoxin 1.
GN	PRDX2 OR PRX1.
RC	STRAIN=29SVJ;
RX	MEDLINE=9838288; PubMed=9714804;
RA	Lim M.-J., Chae H.-Z., Rhee S.-G., Yoo D.-Y., Lee K.-K., Yeom Y.-I.; "The type II peroxiredoxin gene family of the mouse: molecular structure, expression and evolution.", Gene 216:197-205 (1998).
DR	EMBL: AF032722; AAC35744.1; -
DR	EMBL: AF032718; AAC35744.1; JOINED.
DR	EMBL: AF032719; AAC35744.1; JOINED.
DR	EMBL: AF032720; AAC35744.1; JOINED.
DR	EMBL: AF032721; AAC35744.1; JOINED.
DR	MGI: MGI:109486; Prdx2.
DR	InterPro: IPR00086; AhpC-TSA.
PFam	PF00578; AhpC-TSA; 1.
SO	SEQUENCE 198 AA; 21791 MW; EEFBF0F5426F7174D CRC64;
Query Match	50.5%; Score 727; DB 11; Length 198;
Best Local Similarity	69.4%; Pred. No. 8. 3e-62;
Matches	134; Conservative 23; Mismatches 36; Indels 0; Gaps 0;
Query	79 AKISKPAPWEGAVIDGEFKEKLTDYRGKVIVFFYPLDFPVFCPEIAGDRLE 138
Db	6 AQIGKSAPDTAVVDFGAFKEKLTDYRGKVIVFFYPLDFPVFCPEIAGDRLE 65
QY	139 RSTINTEVACSVDSQFTHAWINWPRROGGGLDRIPLSLDTHQISKDGYVLEDSGHT 198
Db	66 RKGCEVILGVSYDSQFTHAWINWPRROGGGLDRIPLSLDTHQISKDGYVLEDSGHT 125
QY	199 LRLGLFIIDDKGILRQITNDLPGVRSYDTELRLVQAFQYTDKGEVCPAGWPGSETI 258
Db	126 YRLGLFIIDAKGVILRQITNDLPGVRSYDTELRLVQAFQYTDKGEVCPAGWPGSETI 185
QY	259 DPAGKLKFDFK 271

Qy	257	IPDPAGKLKYFDK	269	RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T.,
				RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Db	185	KPDVQOSKDYFSK	197	RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
				RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
				RA	Kuehl P., Lewis S., Matsuo S., Nakauchi T., King B., Kochiwa H.,
				RA	Schriml L.M., Staubli F., Suzuki S., Tomita M., Wagner L., Washio T.,
				RA	Saito K., Okido T., Furuno M., Aono H., Batalov R., Barish G.,
				RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
				RA	Brownstein M.J., Built C., Fletcher C., Fujita M., Gariboldi M.,
				RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
				RA	Lyon P., Marchionni L., Machina J., Mazzarelli C., Monbret P.,
				RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
				RA	Sasaki H., Sato K., Schoenwald C., Sejyo T., Shibata Y., Storch K.-F.,
				RA	Suzuki H., Toyoko K., Wang K.H., Weitz C., Whittaker C., Wilmung L.,
				RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kotsuiki S.,
				RA	Yasashizaki Y.,
				RT	"Functional annotation of a full-length mouse cDNA collection.";
				RL	Nature 409:685-690 (2001).
				DR	EMBL: AK01688; BAB27120; 1; -
				DR	HSSP; P30041; IPRX.
				DR	MGD; MG1:9523; Prdx1.
				DR	InterPro; IPR000666; AhpC-TSA.
				DR	Pfam; PF00578; AhpC-TSA; 1.
				SQ	SEQUENCE 199 AA; 22236 MW; BBEF5C989D86124D1 CRC64;
					Query Match 49.9%; Score 718.5; DB 11; Length 199;
					Best Local Similarity 68.8%; Pred. No. 5.5e-61;
					Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps
					6 AKIGYPPAPNPKATAVMPDFGKFDKDISSEYKGKVVFFYPLDFPVCPTTEIAFGRLEE 137
					DB 65 FRKLNQCVIGASVSDHSFCHLAWINTPKRQGGLGPMLNPLISDPKPKTAQDGVLKADEGI 125
					Qy 79 AKTSKISKAPYWECHAVI-DGEFFKELKLTIDYRGKLYVFFYPLDFPVCPTTEIAFGRLEE 137
					Qy 138 FRSINTEVVAVASVSDQSTHLMINTPRQGGGPRLPLSPLTHDISKQGVYLDSDH 197
					DB 66 FRKLNQCVIGASVSDHSFCHLAWINTPKRQGGLGPMLNPLISDPKPKTAQDGVLKADEGI 125
					Qy 198 TLRGLFLIDDKGILRQITLNDLPGVRSDEURLVQAFQYTDKHGKGVCPAGWKPGSETII 257
					DB 126 SFRGLFLIDDKGILRQITLNDLPGVRSDEURLVQAFQYTDKHGKGVCPAGWKPGSETII 185
					Qy 258 PDPAKLKYFDK 269
					DB 186 PDVNKSKYFFK 197
					RESULT 14
					ID 09DB49 PRELIMINARY; PRT: 198 AA.
					AC 09DB49; DT 01-JUN-2001 (TREMBrel. 17, Created)
					DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
					DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
					DE Peroxiredoxin 2.
					GN PRDX2.
					OS Mus musculus (Mouse).
					OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
					OC NCBI_TaxID=10090;
					RN 1
					SEQUENCE FROM N.A.
					RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;
					RC MEDLINE=21085660; PubMed=1217851;
					RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
					RA Arakawa T., Hara A., Fukunishi Y., Kondo H., Adachi J., Fukuda S.,
					RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T.,
					RA Saito T., Okazaki Y., Gorobori T., Bono H., Kasukawa T., Saito R.,
					RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
					RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
					RA Kuehl P., Lewis S., Matsuo S., Nakauchi T., King B., Kochiwa H.,
					RA Schriml L.M., Staubli F., Suzuki S., Tomita M., Wagner L., Washio T.,
					RA Sakai K., Okido T., Furuno M., Aono H., Batalov R., Barish G.,
					RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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					RA Sakai K., Okido T., Furuno M., Aono H., Batalov R., Barish G.,
					RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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					RA Kuehl P., Lewis S., Matsuo S., Nakauchi T., King B., Kochiwa H.,
					RA Schriml L.M., Staubli F., Suzuki S., Tomita M., Wagner L., Washio T.,
					RA Sakai K., Okido T., Furuno M., Aono H., Batalov R., Barish G.,
					RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
					RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
					RA Kuehl P., Lewis S., Matsuo S., Nakauchi T., King B., Kochiwa H.,
					RA Schriml L.M., Staubli F., Suzuki S., Tomita M., Wagner L., Washio T.,
					RA Sakai K., Okido T., Furuno M., Aono H., Batalov R., Barish G.,
					RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
					RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
					RA Kuehl P., Lewis S., Matsuo S., Nakauchi T., King B., Kochiwa H.,
					RA Schriml L.M., Staubli F., Suzuki S., Tomita M., Wagner L., Washio T.,
					RA Sakai K., Okido T., Furuno M., Aono H., Batalov R., Barish G.,
					RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
					RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

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GenCore version 5.1.3
GennCore version 5.1.3

OM protein - protein search, using sw model.

Run on: January 17, 2003, 19:15:02 ; Search time 11 Seconds

1021.826 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441

Sequence: 1 MEALPLLAATPDHGRHRL... GSETTIPDPAGKLKYFDKLN 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	271	1 PDX4_HUMAN	Q13162 homo sapien
2	1295	89.9	274	1 PDX4_BOVIN	Q9bq12 bos taurus
3	1262.5	87.6	274	1 PDX4_MOUSE	Q9bg07 mus musculus
4	749	52.0	199	1 PDX2_BOVIN	Q9bg13 bos taurus
5	749	51.8	198	1 PDX2_HUMAN	P32119 homo sapien
6	744	51.6	198	1 PDX2_RAT	P35704 rattus norvegicus
7	735.5	51.0	199	1 PDX1_HUMAN	Q06830 homo sapien
8	732	50.8	198	1 PDX2_MOUSE	Q9bq17 mus musculus
9	731.5	50.8	200	1 PDX2_CYNPY	Cynops pyrrhodon
10	730.5	50.7	199	1 PDX1_RAT	Q63716 rattus norvegicus
11	721.5	50.1	199	1 PDX1_MOUSE	P35700 mus musculus
12	703	48.8	256	1 PDX3_HUMAN	P30048 homo sapien
13	691	48.0	257	1 PDX3_BOVIN	P35705 bos taurus
14	689	47.8	257	1 PDX3_MOUSE	P20108 mus musculus
15	667	46.3	199	1 PDX2_BRUMA	Q17172 brugia malayi
16	660	45.8	200	1 PDX1_ONCNY	Q91191 oncorthynchus
17	639.5	44.4	226	1 TDX1_GAELL	Q21824 caenorhabditis
18	631.5	43.8	199	1 TDX_TYBVR	Q26995 trypanosoma
19	592.5	41.9	210	1 BAS1_HORVU	Q96468 hordeum vulgare
20	589	40.9	196	1 TSAL1_CANAL	Q9Y7F0 candida albicans
21	588.5	40.8	210	1 BAS1_WHEAT	P80602 triticum aestivum
22	584	40.5	195	1 TSAL1_YEAST	P34760 saccharomyces
23	582.5	40.4	265	1 BAS1_SP101	Q24364 spinacia
24	571	39.6	266	1 BAS1_ARATH	Q96791 arabidopsis
25	570.5	39.6	200	1 T7553_YEAST	Q55624 synechocystis
26	567	39.3	195	1 TSD2_YEAST	Q04120 saccharomyces
27	561	38.9	194	1 TDX_FASHE	P91883 fasciola hepatica
28	556.5	38.6	229	1 TDX1_BRUMA	P48822 brugia malayi
29	548	38.0	199	1 YC2_PORPU	P51272 porphyra
30	489	33.9	127	1 PDX2_PIG	P52552 sus scrofa
31	479.5	33.3	233	1 CR29_ENTHI	P19776 entamoeba
32	477	33.1	178	1 R20K_CLOPA	P23161 clostridium
33	404	28.0	198	1 TSAA_HELPY	P56876 helicobacte

ALIGNMENTS

RESULT 1	PDX4_HUMAN	STANDARD;	PRT;	271 AA.
ID	PDX4_HUMAN			
AC	Q13162;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Peroxiredoxin 4 (EC 1.11.1.-) (Prx-IV) (thioredoxin peroxidase A0372)			
DE	(Thioredoxin-dependent peroxide reductase A0372) (Antioxidant enzyme A0372) (AOE372)			
DE	PRDX4.			
GN				
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo; NCBITaxonID=9606;			
OX				
RP				
RX				
RA	Jin D -Y., Chae H.Z., Rhode S.G., Jeang K.-T.;			
RA	"Regulatory role for a novel human thioredoxin peroxidase in NF-kappaB activation";			
RT	J. Biol. Chem. 272:30952-30961(1997).			
RL				
RN	[2]			
RP				
SEQUENCE FROM N.A.				
RA	Strasbourg R.;			
RA	SEQUENCE=Brain;			
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	OVEROXIDATION OF CIS-124.			
RA	Rabilloud T.;			
RL	Unpublished observations (JUL-2002).			
CC	-!- FUNCTION: Probably involved in redox regulation of the cell.			
CC	-!- Regulates the activation of NF-kappa-B in the cytosol by a modulation of I-kappa-B-alpha phosphorylation.			
CC	-!- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked, upon oxidation (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- MISCELLANEOUS: The active site is the redox-active Cys-124 (to CYS-SOH) upon oxidative stress.			
CC	-!- SIMILARITY: BELONGS TO THE AHPC/TS4 FAMILY.			
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CC	EMBL: U25182; AAB95175.1; -.			
DR	EMBL: BC003609; AAH03609.1; -.			

DR	EMBL; BC01770; AAH07107.1; -
DR	HSSP; P30041; IPRX.
DR	GeneID; 17169; PRDX4.
MM	606506; -
DR	InterPro; IPR000866; AhpC-TSA.
DR	Pfam; PF00578; AhpC-TSA; 1.
DR	Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
FT	DOMAIN 20 POLY-LIPO.
ACT SITE	124 REDOX-ACTIVE.
FT	DISULFID 124 INTERCHAIN (PARTIAL) (BY SIMILARITY).
SEQUENCE	271 AA; 30540 MW; 7E5B580049FC60F CRC64;
Query Match	100 %; Score 1441; DB 1; Length 271; Best Local Similarity 100.0%; Pred. No. 4.7e-126; Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 MEALPILAAATPDHGRIRRLLPLPLFLPLDAGAVOGWETEPRTREECFYAGQVY 60
Qy	61 PGEASRVSDAHLHLSSKAKISKPAKYWEAVAVDGFKEKLTLDYRGKVLYFFFYPLDF 120
Db	61 PGEASRVSDAHLHLSSKAKISKPAKYWEAVAVDGFKEKLTLDYRGKVLYFFFYPLDF 120
Qy	121 TFVCPEILFGDRLEFRSINTEVWACSDQSFTHLAWINTPRROGLGPIRPLSDL 180
Db	121 TFVCPEILFGDRLEFRSINTEVWACSDQSFTHLAWINTPRROGLGPIRPLSDL 180
Qy	181 THQISKDGYGLLEDSGHTLRLFLIDDKGILRQITLNDLPGVRSVDETLRLVQAFQYTDK 240
Db	181 THQISKDGYGLLEDSGHTLRLFLIDDKGILRQITLNDLPGVRSVDETLRLVQAFQYTDK 240
Qy	241 HGEVCPAGWPKPSETIIPDPAGKLKYFDKLN 271
Db	241 HGEVCPAGWPKPSETIIPDPAGKLKYFDKLN 271
RESULT 2	
PDX4_BOVIN	STANDARD; PRT; 274 AA.
ID	PDX4_BOVIN
AC	Q9BGJ2;
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DE	PRDX4.
OS	Bos taurus (Bovine).
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovine; Bos.
OX	NCBI_TaxID:9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RA	Leysens G., Donnay I., Knoops B.;
RT	"Cloning of 4 new bovine peroxiredoxins, and screening of the complete peroxiredoxin family in different bovine tissues.";
RT	Submissions (SEP-2000) to the EMBL/GenBank/DBJ databases.
-I	FUNCTION: Probably involved in redox regulation of the cell.
CC	Regulates the activation of NF-kappa-B in the cytosol by a modulation of I-kappa-B-alpha phosphorylation (By similarity).
CC	-I SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked, upon oxidation (By similarity).
CC	-I SUBCELLULAR LOCATION: Cyttoplasmic (By similarity).
CC	-I MISCELLANEOUS: The active site is the redox-active Cys-127 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-248-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity).
CC	-I MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-127 (to Cys-SO3H) upon oxidative stress (By similarity).
RESULT 3	
PDX4_MOUSE	STANDARD; PRT; 274 AA.
ID	PDX4_MOUSE
AC	Q08807;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DE	PRDX4.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID:10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRIN-C57BL/6J;
RX	Medline:21121079; PubMed:11229364;
RA	Wong C.M., Chun A.C., Kok K.H., Zhou Y., Fung P.C., Kung H.F.,
RA	Jeang K.-T., Jin D.-Y.;
RT	"Characterization of human and mouse peroxiredoxin IV: evidence for inhibition by Prx-IV of epidermal growth factor- and p53-induced reactive oxygen species.";
RT	Antioxid. Redox. Signal. 2:507-518 (2000).
-I	FUNCTION: Probably involved in redox regulation of the cell.
CC	Regulates the activation of NF-kappa-B in the cytosol by a modulation of I-kappa-B-alpha phosphorylation.
CC	-I SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked,

DR SWISS-2DPAGE; Q06930; HUMAN.
 DR Genew; HGNC; 9352; PRDX1.
 DR MIM; 116763; -.
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 DR Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 KW ACT-SITE 52 52 REDOX-ACTIVE.
 FT DISULFID 52 173 INTERCHAIN (PARTIAL).
 FT CONFLICT 147 147 L -> P (IN REF. 2).
 FT CONFLICT 149 150 VG -> CC (IN REF. 2).
 FT CONFLICT 189 189 O -> P (IN REF. 2).
 FT CONFLICT 191 191 S -> T (IN REF. 2).
 SEQUENCE 199 AA; 22110 MN; 8R68E56D75BF5304 CRC64;

Query Match 51.0%; Score 735.5; DB 1; Length 199;
 Best Local Similarity 70.3%; Pred. No. 6.5e-61;
 Matches 135; Conservative 25; Mismatches 31; Indels 1; Gaps 1;

Db 126 SFRGGFLIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKP 185

QY 258 PDAGKLKYFDK 269

Db 186 PDVQKSKKEYFSK 197

RESULT 8

ID PDX2_MOUSE STANDARD; PRT; 198 AA.
 AC Q61171; Q60796; 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxiredoxin 2 (EC 1.11.1.1) (Thioredoxin-dependent peroxiredoxin 1) (Thiol-specific antioxidant protein) (TSA).
 DE PRDX2 OR TPX.
 OC Mus musculus (Mouse);
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus. OX NCBI_TAXID=10090; RN [1];
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE-97238626; PubMed=9115640;
 RA Ichimura S., Davis J.G., O'Rourke D.M., Katsumata M., Greene M.I.;
 RT "Murine thioredoxin peroxidase delays neuronal apoptosis and is expressed in areas of the brain most susceptible to hypoxic and ischemic injury.";
 RT DNA Cell Biol. 16:311-321(1997).
 RN [2];
 RP SEQUENCE FROM N.A.
 RC STRAIN="129;
 RA Oberbaumer I.;
 RL Submitted (sep-1996) to the EMBL/GenBank/DBJ databases.
 RN [3];
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Chae H.Z., Kim H., Rhee S.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC - FUNCTION: Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system. It is not able to receive electrons from glutaredoxin. May play an important role in eliminating peroxides.

CC CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity).
 CC CC -!- SUBCELLULAR LOCATION: cytoplasmic.
 CC CC -!- TISSUE SPECIFICITY: Widely expressed with highest levels in bone marrow. High levels also found in heart, brain, kidney and skeletal muscle. Lower levels in liver, lung and thymus.
 CC CC -!- MISCELLANEOUS: The active site is the redox-active Cys-51 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-172-SH of the other subunit to form an intermolecular disulfide with a concomitant reduction of the disulfide by thioredoxin (By similarity).
 CC CC -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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DR EMBL; US1679; AAB01941; 01-NOV-1997 (Rel. 35, Created)
 DR EMBL; X82067; CA57566; 01-NOV-1997 (Rel. 35, Last sequence update)
 DR EMBL; U20611; AAR59475; 1; 01-NOV-1997 (Rel. 35, Last sequence update)
 DR HSSP; P32041; 1PRX.
 DR SWISS-2DPAGE; 061171; MOUSE.
 DR MGD; MGI; 109486; Prdx2.
 DR InterPro; IPR000866; AhpC-TSA.
 DR Pfam; PF00578; AhpC-TSA; 1.
 DR Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 KW ACT-SITE 51 51 REDOX-ACTIVE (BY SIMILARITY).
 FT DISULFID 51 172 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 FT CONFLICT 97 97 G -> A (IN REF. 3).
 FT CONFLICT 182 182 T -> N (IN REF. 3).
 SEQUENCE 198 AA; 21778 MN; FE21685426F7174D CRC64;

Query Match 50.8%; Score 732; DB 1; Length 198;
 Best Local Similarity 69.9%; Pred. No. 1.4e-60;
 Matches 135; Conservative 23; Mismatches 35; Indels 0; Gaps 0;

Db 6 RKLGEVILGVSVSOFTHLAWINTPRKGGLGPNLPLAVDVTKSLSQNYGVLKNDREGIA 125

QY 79 AKISKPAPWGVAVIDGKELKLTDRGKLVFEEFPLDFTVCFTEIAFGDRLIEF 138

Db 6 AQGKSADFTATAVDCAFEKKEKLSDRKGKVYVLFYPLDFVCPTEIAFSDAHEDF 65

QY 139 RSINTEVVACVSQFTHLAWINTPRROGGLGPIRPLSLTHQISKDSYLEDGHT 198

Db 66 RKLGEVILGVSVSOFTHLAWINTPRKGGLGPNLPLAVDVTKSLSQNYGVLKNDREGIA 125

QY 199 LRGFLIIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWKPGSETIP 258

Db 126 YRGLFLIDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDKHGEVCPAGWKPGSDTIKP 185

QY 259 DRAGKLKYFDKLN 271

Db 186 NVDSKEVFSKHN 198

RESULT 9

ID TDX_CYNPY STANDARD; PRT; 200 AA.
 AC Q90384; 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thioredoxin peroxidase (Thioredoxin-dependent peroxide reductase)
 DE (Animal blastoma protein, 25 kDa) (ABP-25).
 OS Cyano pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ID PDX1_MOUSE STANDARD: PRT; 199 AA.
 AC P35700; DR EMBL:AB023563; BAA86992.1; JOINED.
 DT 01-JUN-1994 (Rel. 29, Created) DR PIR: A48313; A48513.
 DT 01-JUN-1994 (Rel. 29, Last sequence update) DR PIR: JC2259; JC2259.
 DT 15-JUN-2002 (Rel. 41, Last annotation update) DR HSSP: P30041; 1-PRX.
 DE Peroxiredoxin 1 (EC 1.11.1.-) (thioredoxin-dependent peroxide reductase 2) (osteoblast specific factor 3) (OSF-3) DR SWISS-2DPAGE: P35700; MOUSE.
 DE (Macrophage 23 kDa stress protein) DR MGD: MGI:99522; Prx1.
 DE PRDX1 OR TDPX2 OR MSP23 OR PRGA. DR InterPro: IPR00866; Apnc-TSA.
 DE Mus musculus (Mouse) DR Pfam: PF00578; Apnc-TSA; 1.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; DR KW Antioxidant; Peroxidase; Redox-active center.
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. DR FT DISULFID 52 173 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 OC NCBI-TaxID:10090; DR SQ SEQUENCE 199 AA: 22176 MW: BEP5935A86124D1 CRC64.
 RN [1] DR
 RP SEQUENCE FROM N.A. DR
 RC TISSUE=Peritoneal macrophage; DR
 RX MEDLINE:9336671; PubMed=8360158; DR
 RA Ishii T., Yamada M., Sato H., Matsue M., Taketani S., Nakayama K., DR
 RA Sugita Y., Banno S.; DR
 RT "Cloning and characterization of a 23-kDa stress-induced mouse peritoneal macrophage protein." DR
 RT J. Biol. Chem. 268:18633-18636(1993). DR
 RL [2] DR
 RP SEQUENCE FROM N.A. DR
 RC STRAIN=C3BL6; TISSUE=osteoblast; DR
 RA Kawai S., Takeshita S., Okazaki M., Kikuno R., Kudo A., Amann B.; DR
 RT "Cloning and characterization of OSF-3, a new member of the MER5 family, expressed in mouse osteoblastic cells." DR
 RL J. Biol. Chem. 115:61-643(1994). DR
 RN [3] DR
 RP SEQUENCE FROM N.A. DR
 RC STRAIN=129/SvJ; TISSUE=Liver; DR
 RA Hino K., Sato H., Banno S.; DR
 RT "Characterization of mouse type I peroxiredoxin gene and pseudogenes." DR
 RT Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. DR
 CC -1- FUNCTION: Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system but not from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2). DR
 CC -1- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity). May form heterodimers with AOP2. DR
 CC -1- SUBCELLULAR LOCATION: Cyttoplasmic. DR
 CC -1- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES; HIGH CONCENTRATION IN LIVER. DR
 CC -1- INDUCTION: BY OXIDATIVE AND SULPHYDRYL-REACTIVE AGENTS. DR
 CC -1- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity). DR
 CC -1- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52 (to Cys-SOH) upon oxidative stress (By similarity). DR
 CC -1- SIMILARITY: BELONGS TO THE AOP1/MSA FAMILY. DR
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 CC EMBL; D16142; BAA03713.1; DR
 DR D21252; BAA04796.1; DR
 DR EMBL; AB023564; BAA86992.1; JOINED. DR
 DR EMBL; AB023360; BAA86992.1; JOINED. DR
 DR EMBL; AB023561; BAA86992.1; JOINED. DR
 DR EMBL; AB023562; BAA86992.1; JOINED. DR
 DR EMBL; AB023563; BAA86992.1; JOINED. DR
 DR EMBL; AB023564; BAA86992.1; JOINED. DR
 DR EMBL; AB023565; BAA86992.1; JOINED. DR
 DR EMBL; AB023566; BAA86992.1; JOINED. DR
 DR EMBL; AB023567; BAA86992.1; JOINED. DR
 DR EMBL; AB023568; BAA86992.1; JOINED. DR
 DR EMBL; AB023569; BAA86992.1; JOINED. DR
 DR EMBL; AB023570; BAA86992.1; JOINED. DR
 DR EMBL; AB023571; BAA86992.1; JOINED. DR
 DR EMBL; AB023572; BAA86992.1; JOINED. DR
 DR EMBL; AB023573; BAA86992.1; JOINED. DR
 DR EMBL; AB023574; BAA86992.1; JOINED. DR
 DR EMBL; AB023575; BAA86992.1; JOINED. DR
 DR EMBL; AB023576; BAA86992.1; JOINED. DR
 DR EMBL; AB023577; BAA86992.1; JOINED. DR
 DR EMBL; AB023578; BAA86992.1; JOINED. DR
 DR EMBL; AB023579; BAA86992.1; JOINED. DR
 DR EMBL; AB023580; BAA86992.1; JOINED. DR
 DR EMBL; AB023581; BAA86992.1; JOINED. DR
 DR EMBL; AB023582; BAA86992.1; JOINED. DR
 DR EMBL; AB023583; BAA86992.1; JOINED. DR
 DR EMBL; AB023584; BAA86992.1; JOINED. DR
 DR EMBL; AB023585; BAA86992.1; JOINED. DR
 DR EMBL; AB023586; BAA86992.1; JOINED. DR
 DR EMBL; AB023587; BAA86992.1; JOINED. DR
 DR EMBL; AB023588; BAA86992.1; JOINED. DR
 DR EMBL; AB023589; BAA86992.1; JOINED. DR
 DR EMBL; AB023590; BAA86992.1; JOINED. DR
 DR EMBL; AB023591; BAA86992.1; JOINED. DR
 DR EMBL; AB023592; BAA86992.1; JOINED. DR
 DR EMBL; AB023593; BAA86992.1; JOINED. DR
 DR EMBL; AB023594; BAA86992.1; JOINED. DR
 DR EMBL; AB023595; BAA86992.1; JOINED. DR
 DR EMBL; AB023596; BAA86992.1; JOINED. DR
 DR EMBL; AB023597; BAA86992.1; JOINED. DR
 DR EMBL; AB023598; BAA86992.1; JOINED. DR
 DR EMBL; AB023599; BAA86992.1; JOINED. DR
 DR EMBL; AB023600; BAA86992.1; JOINED. DR
 DR EMBL; AB023601; BAA86992.1; JOINED. DR
 DR EMBL; AB023602; BAA86992.1; JOINED. DR
 DR EMBL; AB023603; BAA86992.1; JOINED. DR
 DR EMBL; AB023604; BAA86992.1; JOINED. DR
 DR EMBL; AB023605; BAA86992.1; JOINED. DR
 DR EMBL; AB023606; BAA86992.1; JOINED. DR
 DR EMBL; AB023607; BAA86992.1; JOINED. DR
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